

APPLICANT: Ruoslahti, Erkki
 APPLICANT: Koivunen, Erkki
 TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/286,861
 FILING DATE: 04-AUG-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9992
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 TOPOLOGY: Circular
 US-08-286-861-7

Query Match 100.0%; Score 35; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 15
 US-08-924-002-1
 ; Sequence 1, Application US/08924002
 ; Patent No. 6177542
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki I.
 ; APPLICANT: Koivunen, Erkki I.
 ; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,002
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/625,695

FILING DATE: 03-APR-1996
 ;
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,186
 ;
 ; FILING DATE: 11-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LA 2748
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-0001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: both
 US-08-924-002-1
 Query Match 100.0%; Score 35; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Mismatches 0;
 Matches 5; Conservative 0; Gaps 0;
 Qy 1 CRGDC 5
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 Db 1 CRGDC 5

Search completed: September 22, 2004, 07:02:53
 Job time : 34 secs

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COUNTRY: USA ; INFORMATION FOR SEQ ID NO: 1:
ZIP: 92122 ; SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM: ; LENGTH: 6 amino acids
MEDIUM TYPE: Floppy disk ; TYPE: amino acid
COMPUTER: IBM PC compatible ; TOPOLOGY: both
OPERATING SYSTEM: PC-DOS/MS-DOS ; US-08-625-695A-1

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,238
FILING DATE: Query Match 100.0%; Score 35; DB 2; Length 6;
CLASSIFICATION: 514 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 9775
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS: 4:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-425-238-4

Query Match 100.0%; Score 35; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13
US-08-625-695A-26
Sequence 26, Application US/08625695A
; GENERAL INFORMATION:
; Patent No. 591234
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki I.
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,695A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-625-695A-26

Query Match 100.0%; Score 35; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
US-08-386-861-7
Sequence 7, Application US/08286861
; GENERAL INFORMATION:
; Patent No. 5984478
; ATTORNEY/AGENT INFORMATION:
; CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEX: (619) 535-8949
; GENERAL INFORMATION:

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OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/924,002
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/625,695
 FILING DATE: 03-APR-1996
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,186
 FILING DATE: 11-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 2748
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 US-08-924-002-10

Query Match 100.0%; Score 35; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 9
 US-08-212-186A-1
 ; Sequence 1, Application US/08212186A
 ; Patent No. 5536814
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki I.
 ; ATTORNEY: Koivinen, Erkki
 ; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/212,186A
 ; FILING DATE: 11-MAR-1994
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LA 9861
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 6 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-212-186A-26

Query Match 100.0%; Score 35; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 11
 US-08-425-238-4
 ; Sequence 4, Application US/08425238
 ; Patent No. 5627263
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; ATTORNEY: Koivinen, Erkki
 ; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California


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; Sequence 8, Application US/08425238
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Koivinen, Erkki
; TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425, 238
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158, 001
; FILING DATE: 24-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31, 815
; REFERENCE/DOCKET NUMBER: P-LA 9775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-425-238-8

Query Match          100.0%; Score 35; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
; Sequence 10, Application US/08625695A
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivinen, Erkki I.
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625, 695A

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; FILING DATE: 03-APR-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212, 186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31, 815
; REFERENCE/DOCKET NUMBER: P-LA 2041
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-625-695A-10

Query Match          100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
; Sequence 42, Application US/08335832
; Sequence 42, Application US/08335832
; Patent No. 5925331
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-Jones, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; TITLE OF INVENTION: Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335, 832
; FILING DATE: 05-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331inan, Kevin E.
; REGISTRATION NUMBER: 35, 303
; REFERENCE/DOCKET NUMBER: 92, 216-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-335-832-42

Query Match          100.0%; Score 35; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model1

Run on: September 22, 2004, 06:51:52 ; Search time 32 Seconds

(without alignments) 8.067 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/.ptodata/2/iaa/5B_COMB.dep;*
3: /cgn2_6/.ptodata/2/iaa/6A_COMB.dep;*
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6: /cgn2_6/.ptodata/2/iaa/backfile1.dep;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	5	1	US-09-212-186A-10
2	35	100.0	5	1	US-08-125-238-8
3	35	100.0	5	2	US-08-125-69A-10
4	35	100.0	5	2	US-08-335-822-42
5	35	100.0	5	2	US-08-753-701-35
6	35	100.0	5	2	US-08-386-861-37
7	35	100.0	5	3	US-09-141-127-15
8	35	100.0	5	3	US-08-924-002-10
9	35	100.0	6	1	US-08-112-186A-1
10	35	100.0	6	1	US-08-924-002-26
11	35	100.0	6	1	US-08-425-238-4
12	35	100.0	6	2	US-08-625-595A-1
13	35	100.0	6	2	US-08-625-595A-26
14	35	100.0	6	2	US-08-286-861-7
15	35	100.0	6	3	US-08-924-002-1
16	35	100.0	6	3	US-08-924-002-26
17	35	100.0	7	3	US-09-426-680-11
18	35	100.0	8	3	US-09-026-633-4
19	35	100.0	9	2	US-08-701-124-3
20	35	100.0	9	2	US-08-701-124-4
21	35	100.0	9	2	US-08-286-861-15
22	35	100.0	9	2	US-08-286-861-16
23	35	100.0	9	2	US-08-286-861-17
24	35	100.0	9	2	US-08-286-861-18
25	35	100.0	9	2	US-08-286-861-19
26	35	100.0	9	3	US-09-026-633-1
27	35	100.0	9	3	US-09-130-225-3

RESULT 1
US-08-212-186A-10
; Sequence 10, Application US/08212186A
; Patent No. 5536314
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; INVENTOR: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,186A
FILING DATE: 11-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 98611
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: both
US-08-212-186A-10

Query Match 100.0% ; Score 35; DB 1; Length 5;
Best Local Similarity 100.0% ; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRGDC 5
Db 1 CRGDC 5

RESULT 2
US-08-425-238-8

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 1
; OTHER INFORMATION: Alanine is attached to DSPE-PEG5k-succinyl
US-10-850-873-10

Query Match Similarity 100.0%; Score 35; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	CRGDC	5
Db	4	CRGDC	8

Search completed: September 22, 2004, 07:04:03
Job time : 66 secS

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; PRIOR APPLICATION NUMBER: US 09/801,485
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO: 2
; SOFTWARE: PatentIn version 3.1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: RGD Peptide
US-10-917-709-2

Query Match      100.0%;  Score 35;  DB 6;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 6.5e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1  CRGDC 5
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Db   3  CRGDC 7

RESULT 12
US-10-712-298-20
; Sequence 20, Application US/10712298
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; ATTORNEY OR AGENT FOR APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/712,298
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/767,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/1548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: peptide
US-10-712-298-20

Query Match      100.0%;  Score 35;  DB 6;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 6.5e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1  CRGDC 5
     |||||
Db   3  CRGDC 7

RESULT 13
US-10-808-758-78
; Sequence 78, Application US/10808758
; GENERAL INFORMATION:
; APPLICANT: Von Segern, Daniel J.
; TITLE OF INVENTION: ADENOVIRUS PARTICLES WITH ENHANCED INFECTIVITY OF DENDRITIC CELLS
; FILE REFERENCE: 22908-1239

; CURRENT APPLICATION NUMBER: US/10/808,758
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/459,000
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: US 60/467,500
; PRIOR FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 78
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CRGD peptide
US-10-808-758-78

Query Match      100.0%;  Score 35;  DB 6;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 1.8e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1  CRGDC 5
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Db   4  CRGDC 8

RESULT 14
US-09-791-524A-14
; Sequence 14, Application US/09791524A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P26,932-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-14

Query Match      100.0%;  Score 35;  DB 5;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2e+05;
Matches 5;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1  CRGDC 5
     |||||
Db   4  CRGDC 8

RESULT 15
US-10-850-873-10
; Sequence 10, Application US/108500873
; GENERAL INFORMATION:
; APPLICANT: Harvie, Pierrot
; ATTORNEY OR AGENT FOR APPLICANT: Paul, Ralph
; ATTORNEY OR AGENT FOR APPLICANT: Cudmore, Sally
; ATTORNEY OR AGENT FOR APPLICANT: O'Mahony, Daniel J.
; TITLE OF INVENTION: LIPID-COMPRISING DRUG DELIVERY COMPLEXES
; FILE REFERENCE: 226272005300
; CURRENT APPLICATION NUMBER: US/10/850,873
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/10/136,187
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: US 60/287,786
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 45

```

Sequence 4, Application US/10729156
; GENERAL INFORMATION:
; APPLICANT: Weng, Shaomeng
; APPLICANT: Yang, Dajun
; TITLE OF INVENTION: Small Molecule Antagonists of BCL-2 Family Proteins
; FILE REFERENCE: UM-08477
; CURRENT APPLICATION NUMBER: US/10/729,156
; CURRENT FILING DATE: 2003-12-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-729-156-4

Query Match	100.0%	Score 35;	DB 6;	Length 9;	
Best Local Similarity	100.0%	Pred. No.	6.5e+05;		
Matches	5;	Mismatches	0;	Indels	0;
					Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 8
US-10-877-930-33
; Sequence 33, Application US/10877930
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/877,930
; CURRENT FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US/09/696,070
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: alpha-five integrin binding motif
US-10-877-930-33

Query Match	100.0%	Score 35;	DB 6;	Length 9;	
Best Local Similarity	100.0%	Pred. No.	6.5e+05;		
Matches	5;	Mismatches	0;	Indels	0;
					Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 9
US-10-900-399-20
; Sequence 20, Application US/10900399
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/900,399
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26

PCT-US04-16382-7

```

Query Match 100.0%; Score 35; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 3
US-09-612-852A-14
; Sequence 14, Application US/09612852A
; GENERAL INFORMATION:
; APPLICANT: CURIEL, DAVID T.
; CURRENT APPLICATION NUMBER: US/10342081
; TITLE OF INVENTION: MODIFIED ADENOVIRUS CONTAINING A FIBER REPLACEMENT PROTEIN
; FILE REFERENCE: 678503-2006-2
; CURRENT APPLICATION NUMBER: US/09/612,852A
; CURRENT FILING DATE: 2000-07-10
; PRIORITY NUMBER: 09/250,580
; PRIOR FILING DATE: 1999-02-16
; PRIORITY NUMBER: 60,074,844
; PRIOR FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Peptide ligand
; OTHER INFORMATION: containing the RGD motif
US-09-612-852A-14

Query Match 100.0%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 4
US-09-791-524A-124
; Sequence 124, Application US/09791524A
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
; FILE REFERENCE: P2-992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; CURRENT FILING DATE: 2001-02-22
; PRIORITY NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIORITY NUMBER: US 6,0/098,028
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-124

Query Match 100.0%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 5
US-10-342-081-76
; Sequence 76, Application US/10342081
; GENERAL INFORMATION:
; APPLICANT: Rajopadhye, Milind
; APPLICANT: Edwards, D. Scott
; APPLICANT: Barrett, John A.
; APPLICANT: Carpenter, Jr., Alan P.
; APPLICANT: Harris, Thomas D.
; APPLICANT: Heminway, Stuart J.
; APPLICANT: Liu, Shuang
; APPLICANT: Singh, Prabhakar R.
; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS
; FILE REFERENCE: BMS-2024
; CURRENT APPLICATION NUMBER: US/10/342,081
; CURRENT FILING DATE: 2003-01-14
; PRIORITY NUMBER: US 09/599,295
; PRIORITY NUMBER: 2000-06-21
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-342-081-76

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 6
US-10-815-514-33
; Sequence 33, Application US/10815514
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mae
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 31488
; CURRENT APPLICATION NUMBER: US/10/815,514
; CURRENT FILING DATE: 2004-03-31
; PRIORITY NUMBER: US/09/696,872
; PRIORITY NUMBER: 2000-10-26
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatSeq For Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: alpha-five integrin binding motif
US-10-815-514-33

Query Match 100.0%; Score 35; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 7
US-10-729-156-4

```

Result No.	Score	Query Match Length	DB ID	Description
1	35	100.0	7	US-09-791-524A-148 Sequence 148, App
2	35	100.0	9	PCT-US04-16382-7 Sequence 7, App
3	35	100.0	9	US-09-612-852A-14 Sequence 14, App
4	35	100.0	9	US-09-791-524A-124 Sequence 124, App
5	35	100.0	9	US-10-342-091-76 Sequence 76, App
6	35	100.0	9	US-10-815-514-33 Sequence 33, App
7	35	100.0	9	US-10-729-156-4 Sequence 4, App
8	35	100.0	9	US-10-817-910-33 Sequence 20, App
9	35	100.0	9	US-10-900-399-20 Sequence 34, App
10	35	100.0	9	US-10-912-764-34 Sequence 2, App
11	35	100.0	9	US-10-917-709-2 Sequence 20, App
12	35	100.0	9	US-10-712-288-20 Sequence 78, App
13	35	100.0	10	US-10-808-758-78 Sequence 14, App
14	35	100.0	11	US-09-791-524A-14 Sequence 10, App
15	35	100.0	11	US-10-850-873-10 Sequence 14, App
16	35	100.0	11	US-10-850-873-14 Sequence 27, App
17	35	100.0	11	US-10-869-131-27 Sequence 35, App
18	35	100.0	11	US-10-912-754-35 Sequence 1, App
19	35	100.0	11	US-10-917-709-1 Sequence 315, App
20	35	100.0	12	US-10-637-619-282 Sequence 316, App
21	35	100.0	12	US-10-627-619-315 Sequence 13, App
22	35	100.0	12	US-10-627-619-316 Sequence 13, App
23	35	100.0	13	US-09-791-524A-13 Sequence 23, App
24	35	100.0	13	US-09-791-524A-23 Sequence 22, App
25	35	100.0	15	US-09-791-524A-22 Sequence 16, App
26	35	100.0	16	US-10-917-709-10 Sequence 16, App

RESULT 14
 Sequence 92, Application US/07961889
 GENERAL INFORMATION:
 US-07-961-889-92
 Sequence 92, Application US/07961889
 APPLICANT: Lobl, Thomas J.
 APPLICANT: Chiang, Shiu-Jan
 APPLICANT: Cardarelli, Pina M.
 TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 NUMBER OF SEQUENCES: 223
 CURRENT ADDRESS:
 ADDRESSEE: Spensley Horn Jubas & Lubitz
 STREET: 1880 Century Park East, Fifth Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90067
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/961,889
 FILING DATE: 04-JUN-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/550,330
 FILING DATE: 09-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Bostich, June M.
 REGISTRATION NUMBER: 31,238
 REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 TELEFAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 92:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TOPOLGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Disulfide-bond
 LOCATION: 2..6
 US-08-575-461-92
 Query Match 100.0%; Score 35; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: /note= "Residue 1 is 1-adamantanecacetic acid."
 FEATURE:
 NAME/KEY: Disulfide-bond
 LOCATION: 2..6
 US-07-961-889-92
 Query Match 100.0%; Score 35; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OTHER INFORMATION: /note= "Residue 1 is 1-adamantanecacetic acid."
 FEATURE:
 NAME/KEY: Disulfide-bond
 LOCATION: 2..6
 RESULT 15
 US-08-575-461-92
 Sequence 92, Application US/08575461
 GENERAL INFORMATION:
 APPLICANT: Lobl, Thomas J.
 APPLICANT: Chiang, Shiu-Jan
 APPLICANT: Cardarelli, Pina M.

Sequence 9, Application US/09912609
 GENERAL INFORMATION:
 APPLICANT: UNGER, EVAN C.
 APPLICANT: MATSUNAGA, TERRY ONICHI
 APPLICANT: RAMASWAMY, VARADARAJAN
 APPLICANT: ROMANOWSKI, MAREK J.
 TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
 CURRENT APPLICATION NUMBER: US/09/912,609
 CURRENT FILING DATE: 2001-07-25
 PRIOR APPLICATION NUMBER: 09/703,474
 PRIOR FILING DATE: 2000-10-31
 PRIOR APPLICATION NUMBER: 09/418,124
 PRIOR FILING DATE: 2000-01-05
 NUMBER OF SEQ ID NOS: 131
 SOFTWARE: PatentIn Ver. 2.1
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 SEQ ID NO 9

Query Match Score 35; DB 24; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 US-10-304-160-2
 Sequence 2, Application US/10304160
 GENERAL INFORMATION:
 APPLICANT: WICKHAM, THOMAS J
 APPLICANT: KOVESDI, IMRE
 APPLICANT: ROELVINK, PETRUS W
 APPLICANT: EINFIELD, DAVID
 APPLICANT: BROUGH, DOUGLAS E
 APPLICANT: LIZONOVA, ALENA
 TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETTING AN ADENOVIRAL VECTOR
 FILE REFERENCE: 22014B
 CURRENT APPLICATION NUMBER: US/10/304,160
 CURRENT FILING DATE: 2002-11-25
 PRIOR APPLICATION NUMBER: PCT/US01/17391
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: US 09/631,191
 PRIOR FILING DATE: 2000-08-09
 PRIOR APPLICATION NUMBER: US 60/208451
 PRIOR FILING DATE: 2000-05-31
 NUMBER OF SEQ ID NOS: 31
 SOFTWARE: PatentIn Ver. 3.1
 SEQ ID NO 2
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Homo sapiens

Query Match Score 35; DB 29; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 US-10-304-160-2
 Query Match Score 35; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-09-364-597A-17
 Sequence 37, Application US/09364597A
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki
 ATTORNEY: Koivunen, Erkki
 TITLE OF INVENTION: Novel Integrin-Binding Peptides
 NUMBER OF SEQUENCES: 46
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell & Flores LLP
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 ZIP: 92122
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/364,597A
 FILING DATE: 30-JUL-1999
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/286,861
 FILING DATE: 04-AUG-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 3419
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (858) 535-9001
 TELEFAX: (858) 535-8949
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: circular

US-09-364-597A-37
 Query Match Score 35; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 8
 US-09-627-035-10
 Sequence 10, Application US/09627035
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Erkki I.
 KOIVUNEN, ERKKI
 TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/627,035
 FILING DATE: 27-JUL-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/212,186
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9861
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO:10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-627-035-10
 Query Match Score 35; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 9
 US-09-699-679A-24
 Sequence 24, Application US/09699679A
 GENERAL INFORMATION:
 APPLICANT: Unger, Evan C.
 APPLICANT: Shen, Dekang
 APPLICANT: Wu, Guanli
 TITLE OF INVENTION: Novel Targeted Compositions For Diagnostics And Therapeutic Use
 FILE REFERENCE: UNGR1598
 CURRENT APPLICATION NUMBER: US/09/699,679A
 CURRENT FILING DATE: 2000-10-30
 PRIOR APPLICATION NUMBER: 09/218,660
 PRIOR FILING DATE: 1998-12-22
 PRIOR APPLICATION NUMBER: 08/660,032
 PRIOR FILING DATE: 1996-06-06
 PRIOR APPLICATION NUMBER: 08/640,464
 PRIOR FILING DATE: 1996-05-01
 PRIOR APPLICATION NUMBER: 08/497,684
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 24
 LENGTH: 5
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: Synthetic construct

US-09-699-679A-24
 Query Match Score 35; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 10
 US-09-912-609-9
 RESULT 10
 US-09-912-609-9

TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/625,695
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9861
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 US-08-625-695-10

Query Match 100.0%; Score 35; DB 10; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-08-753-781B-45
 Sequence 45, Application US/08753781B
 GENERAL INFORMATION:
 APPLICANT: Markland, Francis S.
 APPLICANT: Bush, Larry R.
 APPLICANT: Swanson, Stephen
 APPLICANT: Sanchez, Eladio F.
 TITLE OF INVENTION: Thrombolytic Agents with Antithrombotic Properties
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESS: McDonnell Boehnen Hulbert & Berghoff
 STREET: 300 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,781B
 FILING DATE: 02-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noonan, Kevin E.
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,2056
 TELECOMMUNICATION INFORMATION:

TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/625,695
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: DITI 124.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 603 437 8970
 TELEFAX: 603 437 8977
 COUNTRY: USA
 ZIP: 06806
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,781B
 FILING DATE: 02-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noonan, Kevin E.
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,2056
 TELECOMMUNICATION INFORMATION:

RESULT 6
 US-08-982-981-45
 Sequence 45, Application US/08982981
 GENERAL INFORMATION:
 APPLICANT: Markland Jr., Francis S.
 APPLICANT: Bush, Larry R.
 APPLICANT: Swanson, Stephen
 APPLICANT: Flores Sanchez, Eladio
 TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC
 NUMBER OF SEQUENCES: 54
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Diatide, Inc.
 STREET: 9 Delta Drive
 CITY: Londonderry
 STATE: NH
 COUNTRY: USA
 ZIP: 03053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/982,981
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/753,781
 FILING DATE: 02-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: McDaniels, Patricia A.
 REGISTRATION NUMBER: 33,194
 REFERENCE/DOCKET NUMBER: DITI 124.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 603 437 8970
 TELEFAX: 603 437 8977
 COUNTRY: USA
 ZIP: 06806
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/753,781B
 FILING DATE: 02-DEC-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Noonan, Kevin E.
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,2056
 TELECOMMUNICATION INFORMATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158,001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Hook, Gregory
 REGISTRATION NUMBER: 38,701
 REFERENCE/DOCKET NUMBER: FP-LA 1220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 PCT-US94-13542-37

Query Match Score 35; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-08-575-461-55
 ; Sequence 55, Application US/08575461
 ; GENERAL INFORMATION:
 ; APPLICANT: Lobl, Thomas J.
 ; APPLICANT: Chiang, Shiu-Jan
 ; APPLICANT: Cardarelli, Pina M.
 ; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 ; TITLE OF INVENTION: Compounds
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Spensley Horn Jubas & Lubitz
 ; STREET: 1880 Century Park East, Fifth Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/575,461
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/961,889
 ; FILING DATE: 04-JUN-1993
 ; OPERATING SYSTEM: US 07/550,330
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/575,461
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/961,889
 ; FILING DATE: 09-JUL-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bostich, June M.
 ; REGISTRATION NUMBER: 31,238
 ; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 455-5100
 ; TELEFAX: (619) 455-5110
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Disulfide-bond
 ; LOCATION: 1..5
 ; US-08-575-461-55

Query Match Score 35; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-08-625-695-10
 ; sequence 10, Application US/08625695
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruosahti, Erkki I.
 ; APPLICANT: Koivunen, Erkki

Query Match Score 35; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-07-961-889-55
 ; sequence 55, Application US/07961889
 ; GENERAL INFORMATION:
 ; APPLICANT: Lobl, Thomas J.
 ; APPLICANT: Chiang, Shiu-Jan
 ; APPLICANT: Cardarelli, Pina M.
 ; TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 ; TITLE OF INVENTION: Compounds
 ; NUMBER OF SEQUENCES: 223
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Spensley Horn Jubas & Lubitz
 ; STREET: 1880 Century Park East, Fifth Floor
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90067
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/961,889
 ; FILING DATE: 04-JUN-1993
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/550,330
 ; FILING DATE: 09-JUL-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bostich, June M.
 ; REGISTRATION NUMBER: 31,238
 ; REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 455-5100
 ; TELEFAX: (619) 455-5110
 ; INFORMATION FOR SEQ ID NO: 55:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Disulfide-bond
 ; LOCATION: 1..5
 ; US-07-961-889-55

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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:49:42 ; Search time 430 Seconds
(without alignments)
11.349 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5

Scoring table: BL2SUM62
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues

Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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30: /cgn2_6_ptodata/2/paa/US104_COMB_pep:*
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32: /cgn2_6_ptodata/2/paa/US107_COMB_pep:*
33: /cgn2_6_ptodata/2/paa/US106_COMB_pep:*
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ALIGNMENTS

RESULT 1
PCT-US94-13542-37
; Sequence 37, Application PC/TUS9413542
; GENERAL INFORMATION:
; APPLICANT: La Jolla Cancer Research Foundation
; TITLE OF INVENTION: Novel Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/13542
FILING DATE: 22-NOV-1994
CLASSIFICATION:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	100.0			

; TELEPHONE: (858) 535-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-397A-18

Query Match Similarity 100.0%; Score 35; DB 9; Length 9;
Best Local Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
|||
Db 3 CRGDC 7

Search completed: September 22, 2004, 07:06:15
Job time : 128 secs

RESULT 13
US-09-364-597A-16
Sequence 16, Application US/09364597A
Patent No. US20020103130A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-9949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-09-364-597A-17

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 14
US-09-364-597A-17
Sequence 17, Application US/09364597A
Patent No. US20020103130A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Koivunen, Erkki
TITLE OF INVENTION: No. US20020103130A1 Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy diskible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/09/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:

TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With Pro-Apoptotic Activity
FILE REFERENCE: P-LJ 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FASTSEQ For Windows Version 4.0
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: synthetic peptide
US-09-765-086-1

Qy	1	CRGDC 5	Score 35; DB 9; Length 9;
Db	3	CRGDC 7	Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
US-09-845-160-5
Sequence 5, Application US/09845160
Patent No. US2000058045A1
GENERAL INFORMATION:
APPLICANT: MIZUGUCHI, HIROYUKI
APPLICANT: HAYAKAWA, TAKAO
TITLE OF INVENTION: ADENOVIRUS VECTOR
FILE REFERENCE: 081356/0163
CURRENT APPLICATION NUMBER: US/09/845,160
CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: JP 2001-131688
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence: RGD-4C peptide
US-09-845-160-5

Qy	1	CRGDC 5	Score 35; DB 9; Length 9;
Db	3	CRGDC 7	Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
US-09-245-603A-16
Sequence 16, Application US/09245603A
GENERAL INFORMATION:
APPLICANT: Curiel, David T.
APPLICANT: Krasnykh, Victor N.
APPLICANT: Dmitriev, Igor
TITLE OF INVENTION: Adenovirus Vector Containing A Heterologous Peptide Epitope in the HI Loop of the Fiber Knob
FILE REFERENCE: D6080
CURRENT APPLICATION NUMBER: US/09/245,603A
CURRENT FILING DATE: 1999-02-05

PRIOR APPLICATION NUMBER: US 60/099,801
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 16
LENGTH: 9
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Amino acid sequence of a RGD peptide incorporated into the region of the fiber gene within the HI loop.
US-09-245-603A-16

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

RESULT 12
US-09-364-597A-15
Sequence 15, Application US/09364597A
Patent No. US200210310A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, E-kki
APPLICANT: KOIVUNEN, ERIKI
TITLE OF INVENTION: No.
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PLA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-09-364-597A-15

Query Match 100.0%; Score 35; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 3 CRGDC 7

US-09-912-609-10
*Sequence 10, Application US/09912609
 Publication No. US0020041888A1*
GENERAL INFORMATION:
APPLICANT: UNGER, EVAN C.
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001-24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/478,124
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 10
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-912-609-10

Query Match 100.0%; Score 35; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 6
 US-09-912-609-13
*Sequence 13, Application US/09912609
 Publication No. US20030041898A1*
GENERAL INFORMATION:
APPLICANT: UNGER, EVAN C.
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001-24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/478,124
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 13
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-912-609-13

Query Match 100.0%; Score 35; DB 12; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 7
 US-09-791-524-148
*Sequence 148, Application US/09791524
 Publication No. US20030143209A1*
GENERAL INFORMATION:
APPLICANT: Avantis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: A3319A
CURRENT APPLICATION NUMBER: US/09/791,524
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/09828
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 148
LENGTH: 7
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524-148

Query Match 100.0%; Score 35; DB 10; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 2 CRGDC 6

RESULT 8
 US-10-013-009-4
*Sequence 4, Application US/10013009
 Publication No. US2002008681A1*
GENERAL INFORMATION:
APPLICANT: McMorris, Trevor C.
APPLICANT: Kelner, Michael J.
TITLE OF INVENTION: Antitumor agents
FILE REFERENCE: 103.008US3
CURRENT APPLICATION NUMBER: US/10/013,009
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 09/386,555
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: US 09/025,633
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 4
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic amino acid sequence
US-10-013-009-4

Query Match 100.0%; Score 35; DB 12; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 2 CRGDC 6

RESULT 9
 US-09-765-006-1
*Sequence 1, Application US/09765086
 Patent No. US0010046498A1*
GENERAL INFORMATION:
APPLICANT: Rhoslantti, Erkki
APPLICANT: Pasqualini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Ellerby, H. Michael

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; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-37

Query Match 100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 2
US-09-912-609-9
; Sequence 9, Application US/09912609
; Publication No. US20041898A1
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMY, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 9 PatentIn Ver. 2.1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-912-609-9

Query Match 100.0%; Score 35; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 3
US-10-304-160-2
; Sequence 2, Application US/10304160
; Publication No. US2003009961A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BIEFIELD, DAVID
; APPLICANT: BROUH, DOUGLAS E
; APPLICANT: LIZONOV, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT FILING DATE: 2002-11-25
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/208451

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 4
US-09-364-597A-7
; Sequence 7, Application US/09364597A
; Patent No. US2002103130A1
; GENERAL INFORMATION:
; APPLICANT: Rugsalanti, Erkki
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: No. US2002103130A1 integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,597A
; FILING DATE: 30-JUL-1999
; CLASIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/158,001
; FILING DATE: 24-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,861
; FILING DATE: 04-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Kathryn
; REGISTRATION NUMBER: 31,815
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (458) 555-9001
; TELEFAX: (858) 535-8949
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-09-364-597A-7

Query Match 100.0%; Score 35; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 5

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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:53:03 ; Search time 127 Seconds

(without alignments)
12.643 Million cell updates/sec

Title: US-09-912-609-9
Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BL05UM62
Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *

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- 2: /cgn2_6/ptodata/1/pubpa/pctus_pubcomb.pep:*
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- 16: /cgn2_6/ptodata/1/pubpa/us10_new_pub.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	35	100.0	5 12 US-09-912-609-9	Sequence 9, Appli
3	35	100.0	5 14 US-10-304-160-2	Sequence 2, Appli
4	35	100.0	6 9 US-09-364-97A-7	Sequence 7, Appli
5	35	100.0	6 12 US-09-912-609-10	Sequence 10, Appli
6	35	100.0	6 12 US-09-912-609-13	Sequence 13, Appli
7	35	100.0	7 10 US-09-791-524-148	Sequence 148, Appli
8	35	100.0	8 12 US-10-013-009-4	Sequence 4, Appli
9	35	100.0	9 9 US-09-765-086-1	Sequence 1, Appli
10	35	100.0	9 9 US-09-845-160-5	Sequence 5, Appli
11	35	100.0	9 9 US-09-245-603A-16	Sequence 16, Appli
12	35	100.0	9 9 US-09-364-597A-15	Sequence 15, Appli
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14	35	100.0	9 9 US-09-364-597A-17	Sequence 17, Appli
15	35	100.0	9 9 US-09-364-597A-18	Sequence 18, Appli

RESULT 1

US-09-164-597A-37
; Sequence 37, Application US/09364597A
; Patent No. US2002010310A1
; GENERAL INFORMATION:
; APPLICANT: Ruoblahti, Erkki
; ATTORNEY/AGENT INFORMATION: Koivunen, Erkki
; TITLE OF INVENTION: No. US2002010310A1 Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

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COMPUTER: IBM PC compatible
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FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/364,597A
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949

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(DIAT-) DIATIDE INC.
 (UYSC-) UNYV SOUTHERN CALIFORNIA.

PA PA
 PA PA
 XX Markland FS, Bush LR, Swenson S, Flores Sanchez E;
 PI PI
 XX DR; WPI: 1998-333336/29.

New thrombolytic agents - comprise thrombolytic proteinase covalently linked to targetting compound for binding to component of thrombus.

PT PT
 PT Linked to targetting compound for binding to component of thrombus.

XX PS
 XX Claim 10: Page 65; 79pp; English.

The invention relates to new thrombolytic agents which comprise a thrombolytic proteinase covalently linked to a targetting compound capable of specifically binding to a component of a thrombus. The thrombolytic agents can be used for eliminating thrombi in vivo in, e.g., myocardial infarction, cerebral ischaemia, deep vein thrombosis or pulmonary embolism. A labelled form of the thrombolytic agent can also be used to image thrombi for diagnostic purposes. The thrombolytic agents are specifically targeted to thrombus sites in vivo and have minimal haemorrhagic side effects and side effects related to non-specific proteolysis. The present sequence represents a specifically claimed targetting peptide. (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 5 AA;

CC Query Match 100.0%; Score 35; DB 2; Length 5;
 CC Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 13
 SQ AAY21570
 ID AAY21570 standard; peptide; 5 AA.
 XX AC AAY21570;
 XX DT 09-AUG-1999 (first entry)
 XX DE Integrin-binding peptide.
 XX KW Integrin; Fibronectin; vitronectin; extracellular matrix protein;
 XX KW metastatic; Fibronectin adhesion; alphasbeta1 integrin.
 XX OS Synthetic.
 XX PN US5912234-A.
 XX PD 15-JUN-1999.
 XX PP 03-APR-1996; 96US-00625695.
 XX PR 27-SEP-1993; 93US-00127422.
 XX PR 11-MAR-1994; 94US-00212186.
 XX PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX PI Koivunen E, Ruoslahti E;
 XX DR WPI; 1999-35721/30.
 XX PT Integrin-binding peptides has specific binding specificity for fibronectin and vitronectin binding integrins.

DISCLOSURE: Col 15; 16pp; English.

The invention relates to peptides having specific binding specificity for fibronectin-binding and vitronectin-binding integrins, and in particular for alphasbeta1 integrin. The peptides can be used in a method of preventing integrin-mediated attachment to an extracellular matrix protein, fibronectin, or vitronectin which comprises (a) contacting the cells with a soluble peptide selected from the sequences shown in AAY21561, AAY21563 and AAY21566; or (b) contacting the cells with a soluble peptide comprising the sequence -NGR- selected from the sequences shown in AAY21564, AAY21566 or AAY21573; or (c) contacting with a soluble peptide shown in AAY21571. The peptides are useful for inhibiting metastatic process with which fibronectin adhesion is associated and also for inhibiting alpha v beta 1-mediated cell attachment to fibronectin, and alpha v beta 5-mediated cell attachment to vitronectin. The peptides are also useful for promoting attachment of integrin expressing cells to a surface or artificial cell matrix. The peptides can be easily and

PA PA
 PA PA
 XX (DIAT-) DIATIDE INC.
 XX Lister-James J, Dean RT;
 PI PI
 XX DR; WPI: 1998-239148/21.

Reagent useful for preparing thrombus imaging agent - comprises peptide covalently linked to technetium binding moiety which is technetium labelled and binds to thrombus component.

RESULT 9
 AAW03492 standard; peptide; 5 AA.
 XX
 ID AAW03492;
 AC
 XX
 DT 25-MAR-2003 (revised)
 DT 24-OCT-1996 (first entry)
 DE Alpha (5)-Beta(1) integrin binding Peptide 10.
 XX
 KW Synthetic; fibronectin; vitronectin; integrin; binding motif; adhesion; extracellular matrix protein; tumour metastasis.
 XX
 OS Synthetic.
 XX
 PN US5536814-A.
 XX
 PD 16-JUL-1996.
 XX
 PP 11-MAR-1994; 94US-00212186.
 XX
 PR 27-SEP-1993; 93US-00127422.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Koivunen E, Ruoslahti E;
 XX
 WPI; 1996-341556/34.
 Synthetic integrin-binding peptide(s) - useful for inhibiting tumour metastasis, etc.
 PS Disclosure; Col 2; 16pp; English.
 XX
 Peptides AAW03483-508 are examples of synthetic peptides generated to bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1). They are synthesised to contain the alpha(5)beta(1)-integrin peptide binding motifs: DGR, NGR or RGD. The peptides interfere with the binding of fibronectin and vitronectin to this integrin and thus may be used to block integrin-mediated cell adhesion to extracellular matrix proteins, esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PP field.)
 XX
 Sequence 5 AA;
 Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 10
 AAW8499
 ID AAW8499 standard; peptide; 5 AA.
 AC
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DB Integrin receptor antagonist peptide 38.
 XX
 KW Integrin receptor antagonist; cell adhesion modulator; leukocyte; extracellular matrix; fibronectin; ARDS; thrombosis; inflammation.
 XX
 OS Synthetic.
 XX
 Key Disulfide-bond 1..5
 FT Location/Qualifiers

XX
 PN US5721210-A.
 XX
 PD 24-FEB-1998.
 XX
 PF 07-JUN-1995; 95US-00485019.
 XX
 PR 09-JUL-1990; 90US-0050330.
 PR 09-JUL-1991; 91US-004862.
 PR 04-JUN-1993; 93US-0051889.
 XX
 PA (TANABE SEIYAKU CO.
 XX
 PI Cardarelli PM, Lohi TJ, Chiang S;
 XX
 DR WPI; 1998-168442/15.
 XX
 PT New cyclic peptide(s) and peptidomimetic compounds - are integrin receptor antagonists useful in modulating cell adhesion.
 PS Example 9; Col 42; 32pp; English.
 XX
 The present sequence represents a synthetic peptide which acts as an antagonist to integrin receptors. The invention provides various synthetic peptides which act as cell adhesion modulators because they mimic extra-cellular matrix ligands or other cell adhesion ligands that bind to receptors such as integrin receptors, including fibronectin, laminin, LFA-1, MAC-1, p150,95, vitronectin and fibrinogen receptors. Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD). Others contain non-RGD sequences, for e.g. RCD sequences, and reverse orientation forms of amino acid residues. The synthetic peptides are useful in modulating cell adhesion, including adhesion related to fibronectin, as well as leukocyte adhesion to endothelial cells. They are also claimed to be useful in the study, diagnosis, treatment or prevention of diseases which relate to cell adhesion, e.g. adult respiratory distress syndrome (ARDS), thrombosis and inflammatory conditions

Sequence 5 AA;
 Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 11
 AAW64952
 ID AAW64952 standard; peptide; 5 AA.
 AC
 XX
 DT 25-MAR-2003 (revised)
 DT 23-SEP-1998 (first entry)
 XX
 DE Targetting peptide #45 useful as component of thrombolytic agent.
 XX
 KW Thrombolytic agent; thrombolytic proteinase; blood clot; fibrin; thrombus; antithrombotic activity.
 XX
 OS Synthetic.
 XX
 PN WO9824917-A1.
 XX
 PD 11-JUN-1998.
 XX
 PR 02-DEC-1997; 97WO-US021918.
 PR 02-DEC-1996; 96US-00753781.

XX	WPI; 1992-313678/38.	Qy	1 CRGDC 5 1 CRGDC 5
XX	New synthetic Peptide lipids or salts - useful as cell migration inhibitors, cell adhesion membranes and cell culture bodies.	Db	
XX	Disclosure: Page 3; 9pp; Japanese.		
XX	The peptide sequence is an example of a highly generic sequence contg. the RGD motif. Compounds contg. these lipid peptides are useful as cell migration inhibitors in cell adhesion membranes or cell culture bodies. See also AAR29048-54		
XX	Sequence 5 AA;		
SQ	Query Match 100.0%; Score 35; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1 CRGDC 5 1 CRGDC 5
Db			
RESULT 7			
AAR69325			
ID AAR69325 standard; peptide; 5 AA.			
XX		Key	Location/Qualifiers
AC AAR69325;	XX	PH	1..5
XX	XX	FT	
DT 25-MAR-2003 (revised)	XX	Disulfide-bond	
DT 25-JUN-1995 (first entry)	XX	PN	W09514714-A1.
XX	XX	PD	01-JUN-1995.
Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.	XX	PP	22-NOV-1994;
XX	XX	PR	24-NOV-1993;
Scintigraphy; thrombus; imaging; specific binding; technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.	XX	PR	04-AUG-1994;
KW	XX	PA	(LUJOL-) LA JOLLA CANCER RES FOUND.
KW	XX	PI	Ruoslahti E, Koivunen E;
OS Synthetic.	XX	DR	WPI; 1995-206899/27.
XX	XX	PS	Example 3; Page 25; 86pp; English.
W09323085-A1.	XX	CC	The sequences given in AAR76185-200 and AAR79073-94 are high affinity integrin binding peptides which bind to various integrins. Peptides which bind to alpha5/beta1 integrins contain the motifs Given in AAR76185-86
XX	XX	CC	and peptides which bind to alpha5/beta3 integrins
PD 25-NOV-1993.	XX	CC	contain the motif given in AAR76187. Alpha5/beta3 integrins are also bound by RGD containing Peptides. These Peptides assume a conformationally stabilized configuration which is due to the formation of a disulphide bond, a peptide bond or a lactam bond. These peptides may be used for isolating the complementary integrin from a sample mixture by contacting them under ionic conditions to allow binding of the integrin to the peptide and then separating the integrin from the peptide. They can be used for attaching cells to a substrate, by binding them to the substrate with the cell. The peptides promote wound healing when applied locally and inhibit the attachment of osteoclasts to bone. They inhibit angiogenesis, metastasis of tumours and migration of smooth muscle cells
XX	XX	CC	Sequence 5 AA;
PF 21-MAY-1993; 93WO-US004794.	XX	CC	Query Match 100.0%; Score 35; DB 2; Length 5;
XX	PR 21-MAY-1992; 92US-00886752.	CC	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX	XX	CC	Mismatches 0; Indels 0; Gaps 0;
PA (DIAT-) DIATECH INC.	XX	Qy	1 CRGDC 5 1 CRGDC 5
XX	PI Dean RT, Lister-James J;	Db	
XX	DR 1993-386229/48.		
XX	Reagent for scintigraphic imaging of thrombi with 99m technetium - PT comprises synthetic peptide which binds to thrombus covalently coupled to metal binding gp., rapidly cleared from blood and tissue.		
XX	PS Claim 46; 61pp; English.		
XX	The invention relates to reagents for scintigraphic imaging of a thrombus in-vivo, comprising (A) a specific binding compound capable of binding to at least one component of a thrombus, covalently linked to (B) a technetium-99m-binding moiety. Specific peptides constituting the reagents are claimed as new. The present peptide is one such peptide. CC reagents are claimed as new. The present peptide is one such peptide. CC (Updated on 25-MAR-2003 to correct PN Field.)		
XX	Sequence 5 AA;		
SQ	Query Match 100.0%; Score 35; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1 CRGDC 5 1 CRGDC 5

XX DT 10-APR-1991 (First entry)
 XX DE Fibrinogen receptor antagonising peptide (VI).
 XX KW Fibrinogen receptor antagonist; platelet aggregation; thrombosis;
 XX myocardial infarction.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Disulfide-bond 1..5
 Modified-site 1..1
 /label= homoCys8

XX FN EP10537-A.
 XX PD 30-JAN-1991.
 XX FT 23-JUL-1990; 90EP-00202015.
 XX PR 28-JUL-1989; 89US-00386534.
 XX PA (MERCK & CO INC.
 PI Nutt RF, Brady SF, Veber DF;
 XX DR 1991-030928/05.
 XX PT New fibrinogen receptor antagonising peptide cpds. - used to inhibit
 blood platelet aggregation during surgery on peripheral arteries and in
 cardiovascular surgery.
 XX PS 7; Page 10; 10pp; English.

XX To residue homocys8 is attached Acetyl and to residue Cys5 is attached
 CC NH2. The peptide is prep. using standard methods of solid phase
 CC synthesis and is one of 17 pre. examples of a highly generic formula.
 CC The peptide is used to inhibit fibrinogen-induced platelet aggregation
 CC and is paricic useful because it does not significantly deplete the
 CC platelet count. It has a relatively short duration of activity and is
 thus useful where prevention of platelet aggregation over a short period
 CC of time is desirable, e.g. in surgery of peripheral arteries and
 CC cardiovascular surgery. It is also useful in prevention of platelet
 CC thrombosis, thromboembolism and reocclusion either during and after
 CC thrombolytic therapy, or after angioplasty of coronary and other arteries
 CC and after coronary artery by-pass procedures, or to prevent myocardial
 CC infarction. It may be combined with thrombolytic agents, e.g. plasminogen
 CC activators or streptokinase, or anticoagulants. See also ARI10413-18 and
 CC EP-410537, EP-410539, EP-410540, EP-410541, and EP-410767
 XX SQ Sequence 5 AA;

XX Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 CRGDC 5
 DB 1 CRGDC 5

XX RESULT 6
 ID AAR29052 standard; Peptide; 5 AA.
 XX PT AAR29052;
 AC AC
 DT 20-MAY-1998 (first entry)
 XX DR 20-MAY-1998 (first entry)
 XX DE Peptide lipid contg. RGD.
 XX KW Synthetic; cell migration; inhibitor; cell adhesion membrane;
 XX cell culture body.

XX Key Location/Qualifiers
 FT modified_site 1
 FT modified_site 5
 /note= "acylated"
 /note= "alkylated"

XX FN JP04221395-A.
 XX PN PD 11-AUG-1992.
 XX PR 29-NOV-1990;
 XX PF 90JP-00333336.
 XX PR 26-OCT-1990;
 XX PA (FUJIF) FUJI PHOTO FILM CO LTD.
 XX DR WPI; 1992-311679/38.

XX PT New Synthetic Peptide lipid(s) and salts - useful as cell migration
 inhibitors, cell adhesion membranes or cell culture bodies.

XX PS Disclosure; Page 3; 9pp; Japanese.

XX CC The peptide sequence is an example of a highly generic sequence contg.
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors in cell adhesion membranes or cell culture bodies.
 See also ARI27027-33

XX SQ Sequence 5 AA;

XX Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 CRGDC 5
 DB 1 CRGDC 5

XX RESULT 6
 ID AAR29052 standard; Peptide; 5 AA.
 XX PT AAR29052;
 AC AC
 DT 20-MAY-1998 (first entry)
 XX DR 20-MAY-1998 (first entry)
 XX DE Peptide lipid contg. RGD.
 XX KW Synthetic; cell migration; inhibitor; cell adhesion membrane;
 XX cell culture body.

XX Key Location/Qualifiers
 FT modified_site 1
 FT modified_site 5
 /note= "acylated"
 /note= "alkylated"

XX FN JP04221394-A.
 XX PN PD 11-AUG-1992.
 XX PR 29-NOV-1990;
 XX PF 90JP-00333335.
 XX PR 26-OCT-1990;
 XX PA (FUJIF) FUJI PHOTO FILM CO LTD.

XX PS Disclosure; Page 3; 9pp; Japanese.

XX CC The peptide sequence is an example of a highly generic sequence contg.
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors. Compounds contg. these lipid peptides are useful as cell
 CC migration inhibitors in cell adhesion membranes or cell culture bodies.
 See also ARI27027-33

XX SQ Sequence 5 AA;

XX Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Qy 1 CRGDC 5
 DB 1 CRGDC 5

XX RESULT 5
 ID AAR27031 standard; Peptide; 5 AA.
 XX AC AAR27031;
 XX DT 20-MAY-1998 (first entry)
 XX DR Peptide lipid contg. RGD.
 XX KW Synthetic; cell migration; inhibitor; cell adhesion membrane;

Copyright (c) 1993 - 2004 Compugen Ltd.	Aam48797	Tumour-ta
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Maximum DB seq length: 2000000000	Aar79073	Alphav/be
Post-processing: Minimum Match 0% Maximum Match 100%	Aar76199	Alphav/be
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3: GeneseqP2000s:*	Aaw56035	Chimeric
4: GeneseqP2001s:*	Aay42255	Synthetic
5: GeneseqP2002s:*	Aay3233	RGD-conta
6: GeneseqP203as:*	Aaw93626	NGR recep
7: GeneseqP203bs:*	Aay48821	Membrane
8: GeneseqP2004s:*		
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		RESULT 1
	ID AAR11587	standard; protein; 5 AA.
	XX	
	AC AAR11587;	
	XX	
	DT 12-JUN-1991	(first entry)
	XX	
	DE Fibronogen receptor antagonist #4.	
	XX	
	KW fibrinogen receptor antagonist; thrombosis; fibrinogen;	
	KW IIb/IIIa receptor.	
	XX	
	OS Synthetic.	
	XX	
	Key	Location/Qualifiers
	PH	Disulfide-bond 1..5
	FT	Modified-site 2
	FT	/label= Arg (phenyl)
	XX	
	PN EP422938-A.	
	XX	
	PD 17-APR-1991.	
	XX	
	PF 11-OCT-1990;	90EP-00311151.
	XX	
	PR 13-OCT-1989;	89US-00421224.
	XX	
	PA (MERCK & CO INC.	
	XX	
	PI Nutt RF, Brady ST, Veber KF, Duggan MF;	
	XX	
	DR WPI: 1991-111423/16.	
	XX	
	PT Polypeptide fibrinogen receptor antagonists - used to prevent thrombosis, e.g. during cardiovascular surgery.	
	XX	
	PS Disclosure; Page 7; 16pp; English.	
	XX	
	CC Cys at position 1 carries an acetyl group. The peptide inhibits binding	
	CC of fibrinogen to the platelet membrane glycoprotein complex IIb/IIIa	
	CC receptor. It may be used to prevent post-operative thrombosis,	
	CC thromboembolism and reocclusion, platelet adhesion in extracorporeal	
	CC blood circulation systems and to prevent myocardial infarction. See also	
	CC AAR11584-6 and AAR11588-R11594	
	XX Sequence 5 AA;	
	SQ	

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Query Match Similarity 100.0%; Score 35; DB 16; Length 477;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 CRGDC 5
          |||||
Db      444 CRGDC 448
```

Search completed: September 22, 2004, 06:54:58
Job time : 117 secs

ATPD. Tropheryma whippelii (Whipple's bacillus) (Tropheryma whippelii). OS Tropheryma whippelii (Whipple's bacillus) (Tropheryma whippelii). OC Bacteria; Actinobacteria; Cellulomonadaceae; Tropheryma. OC Micrococcineae; Cellulomonadaceae; Actinomycetales. NCBI_TaxID=2039; [1]

SEQUENCE FROM N.A.

RA Maiwald M., Lepp P.W., Relman D.A.; RT "Analysis of conserved non-RNA genes of *Tropheryma whippelii*: implications for genome structure, strain typing, and phylogenetic relationships"; RLM submitted (PEB-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; APB3648; AA04483; 1..

GO; GO:004255; C:hydrogen-translocating F-type ATPase complex; IEA.

DR GO; GO:0005524; F:AMP binding; IEA.

DR GO; GO:0005224; F:ATP-binding and phosphorylation-dependent C. . ; IEA.

DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.

DR GO; GO:0015992; P:proton transport; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR000194; ATPase_a/bN.

DR InterPro; IPR004100; ATPase_a/bcentre.

DR InterPro; IPR00793; ATPase_a/bN.

DR InterPro; IPR005722; ATP synthetase_beta.

DR InterPro; IPR0006; ATP-synt_ab_C.

PFam; PF02874; ATP-synt_ab_N; 1.

SMART; SM00382; AAA; 1.

TIGRFAMS; TIGR01039; atpD; 1.

PROSITE; PS00152; ATPase_ALPHA_BETA; 1.

KW Hydrolase; Complete proteome.

SEQUENCE 474 AA; 2D4AD8828A37F4BC CRC64;

Query Match 100.0%; Score 35; DB 16; Length 474; Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;

RESULT 15

Qy 1 CRGDC 5

Db 441 CRGDC 445

Q83691 PRELIMINARY; PRT; 477 AA.

ID Q83691; AC Q83691; DT 01-JUN-2003 (TREMBLrel. 24, Created); DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DR GO; GO:045255; C:hydrogen-translocating F-type ATPase complex; IEA.

DR GO; GO:005524; F:ATP-binding; IEA.

DR GO; GO:008553; F:hydrogen-exporting ATPase activity, phospho. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

DR GO; GO:0016787; F:hydrolyase activity; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.

DR GO; GO:0015993; P:proton transport; IEA.

RA Claverie J.-M.; Audic S.; Robert C.; Ogata H.; Suire K.; Drancourt M.; RT "Tropheryma whippelii illustrates the diversity of gene loss patterns in small genome bacterial pathogens"; RLM submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB016851; AA044521; 1..

DR GO; GO:045255; C:hydrogen-translocating F-type ATPase complex; IEA.

DR GO; GO:005524; F:ATP-binding; IEA.

DR GO; GO:008553; F:hydrogen-exporting ATPase activity, phospho. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0015986; P:ATP synthase coupled proton transport; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR00194; ATPase_a/bcentre.

DR InterPro; IPR004100; ATPase_a/bN.

DR InterPro; IPR00793; ATPase_a/bN.

DR InterPro; IPR0006; ATP-synt_ab_C.

PFam; PF00006; ATP-synt_ab_1.

PFam; PF00306; ATP-synt_ab_C; 1.

PFam; PF02874; ATP-synt_ab_N; 1.

SMART; SM00382; AAA; 1.

TIGRFAMS; TIGR01039; atpD; 1.

PROSITE; PS00152; ATPase_ALPHA_BETA; 1.

KW Hydrolase; Complete proteome.

SEQUENCE 477 AA; 52459 MW; 0001063A50782DE CRC64; SQ

SEQUENCE FROM N.A.

RA Raoult D.; Audic S.; Robert C.; Ogata H.; Suire K.; Drancourt M.; RA

RT "Tropheryma whippelii illustrates the diversity of gene loss patterns in small genome bacterial pathogens"; RLM submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AB016851; AA044521; 1..

DR GO; GO:045255; C:hydrogen-translocating F-type ATPase complex; IEA.

DR GO; GO:005524; F:ATP-binding; IEA.

DR GO; GO:008553; F:hydrogen-exporting ATPase activity, phospho. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

DR GO; GO:0000166; F:nucleotide binding; IEA.

DR GO; GO:0015986; P:ATP synthase coupled proton transport; IEA.

DR InterPro; IPR003593; AAA ATPase.

DR InterPro; IPR00194; ATPase_a/bcentre.

DR InterPro; IPR004100; ATPase_a/bN.

DR InterPro; IPR00793; ATPase_a/bN.

DR InterPro; IPR0006; ATP-synt_ab_C.

PFam; PF00006; ATP-synt_ab_1.

PFam; PF00306; ATP-synt_ab_C; 1.

PFam; PF02874; ATP-synt_ab_N; 1.

SMART; SM00382; AAA; 1.

TIGRFAMS; TIGR01039; atpD; 1.

PROSITE; PS00152; ATPase_ALPHA_BETA; 1.

KW Hydrolase; Complete proteome.

SEQUENCE 477 AA; 52459 MW; 0001063A50782DE CRC64; SQ

SEQUENCE FROM N.A.

RP MEDLINE=22495039; PubMed=12606174;

RX Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A., Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E., von Harby A., Goble A., Rutter S., Squares R., Squares S., Barrell B.G., Parkhill J., Relman D.A.; RT "Sequencing and analysis of the genome of the Whipple's disease bacterium *Tropheryma whippelii*"; RLM submitted (PEB-2003) to the EMBL/GenBank/DDBJ databases.

DR Lancet 367:644 (2003).

DR GO; GO:004555; C:hydrogen-translocating F-type ATPase complex; IEA.

DR GO; GO:000554; F:ATP binding; IEA.

DR GO; GO:0005224; F:ATP-binding and phosphorylation-dependent C. . ; IEA.

DR GO; GO:0008553; F:hydrogen-exporting ATPase activity, phospho. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . ; IEA.

Q8VA50	PRELIMINARY;	PRT;	335 AA.		KW Hypothetical protein, SEQUENCE 336 AA; 37667 MW; FD51D9549357671 CRC64;
AC Q8VA50;				Query Match Score 35; DB 12; Length 279; Best Local Similarity 100.0%; Pred. No. 26;	
DT 01-MAR-2002 (TREMBLrel. 20, Created)				Mismatches 0; Indels 0; Gaps 0;	
DT 01-MAR-2003 (TREMBLrel. 25, Last annotation update)					
DB Glycoprotein (Fragment).					
GN E1.					
OS Ag80-663 virus.					
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;					
OC Alphavirus.					
OX NCBI_TaxID=166978;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE=21465035; PubMed=11581380;					
RA Powers A.M., Brault A.C., Shirako Y., Strauss E.G., Kang W.,					
RA Strauss J.H., Weaver S.C.,					
RT "Evolutionary relationships and systematics of the alphaviruses.";					
RL J. Virol. 75:10118-10131 (2001).					
DR 75:10118-10131.					
DR EMBL; AF398388; AAL35787.1;					
DR GO; GO:0019031; C-viral envelope; IEA.					
DR GO; GO:0005198; F:structural molecule activity; IEA.					
DR InterPro; IPR00548; Alpha_E1_glycop.					
DR InterPro; IPR00336; Flavi_glycoproteE.					
DR InterPro; IPR00710; Ig-like.					
DR PFAM; PF01589; Alpha_E1_glycop; 1.					
FT NON-TER 1					
FT 335					
SQ SEQUENCE 335 AA; 36014 MW; A584EAC07D394BAE CRC64;					
Query Match Score 35; DB 12; Length 335;					
Best Local Similarity 100.0%; Pred. No. 30;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1 CRGDC 5					
Db 286 CRGDC 290					
RESULT 11					
QBNQ07	PRELIMINARY;	PRT;	336 AA.		
AC QBNQ07;					
DT 01-OCT-2002 (TREMBLrel. 22, Created)					
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)					
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)					
DE Hypothetical protein.					
OS Homo sapiens (Human).					
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.					
QX NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC Strausberg R.;					
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.					
DR EMBL; BC029574; AAH29574.1;					
DR GO; GO:005509; F:calcium ion binding; IEA.					
DR GO; GO:004623; F:phospholipase A2 activity; IEA.					
DR GO; GO:0016042; P:lipid catabolism; IEA.					
DR InterPro; IPR01211; PhospholipaseA2.					
DR PROSITE; PS00118; PA2_HIS; 1.					
DR ATP synthase F1 complex beta chain.					
RESULT 12					
Q9CW26	PRELIMINARY;	PRT;	353 AA.		
AC Q9CW26;					
DT 01-JUN-2001 (TREMBLrel. 17, Created)					
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)					
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)					
DB 150016010RIK protein (Fragment).					
GN 150016010RIK.					
OS Mus musculus (Mouse); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;					
NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;					
RX MEDLINE=21085680; PubMed=11217851;					
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
RA Arakawa T., Hara A., Fukunishi H., Konno H., Adachi J.,					
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I.,					
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,					
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Kochiwa H.,					
RA Fleischmann W., Gaasterland T., Giesi C., King B.B., Kochiwa H.,					
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,					
RA Schraml L.M., Staubli F., Suzuki T., Tonita M., Wagner L., Washio T.,					
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,					
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,					
RA Gustenstein M.J., Bult C., Gribaldo M., Garibaldi M., Fujita M.,					
RA Bustamante C., Hill D., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,					
RA Lyons P., Marchionni L., Mashima J., Mazzarilli J., Monbaerts P.,					
RA Nordone P., Ring B., Rinck M., Rodriguez I., Sakamoto N.,					
RA Sasaki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K.-F.,					
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,					
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,					
RA Hayashizaki Y.					
RT "Functional annotation of a full-length mouse cDNA collection.";					
RL Nature 409:685-690 (2001).					
DR EMBL; AK005271; BAB3923.1;					
DR MGD; MGI:1916202; 1500015010RIK.					
DR InterPro; IPR00634; TLLC; 1.					
DR SMART; SM00724; TLLC; 1.					
FT NON-TER	353 AA;	38897 MW;	E989B015AEC83C0A CRC64;		
SEQUENCE					
Query Match Score 35; DB 11; Length 353;					
Best Local Similarity 100.0%; Pred. No. 31;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy 1 CRGDC 5					
Db 284 CRGDC 288					
RESULT 13					
Q84DX6	PRELIMINARY;	PRT;	474 AA.		
AC Q84DX6;					
DT 01-JUN-2003 (TREMBLrel. 24, Created)					
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)					
DB 150016010RIK.					
OC PROSITE; PS00118; PA2_HIS; 1.					

RA Moravec T., Cerovska N., Peccenкова T., Nielsen S. L., Vlcek C.;
 RT "The nucleotide sequence of potato m^op-top isolate 54-15.";
 RL Submitted (NOV-2002) to the ENSEMBL/GenBank/DBJ databases.
 EMBL: AY187010; AA012789.1; -
 DR InterPro; IPR001896; Plant_vir_prot.
 DR Pfam; PF01307; Plant_vir_prot.1.
 SQ SEQUENCE 119 AA; I3154 MW; D2D37E6768305932 CRC64;
 Query Match Score 35; DB 12; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 109 CRGDC 113

RESULT 7
 Q8BMZ3 PRELIMINARY; PRT; 189 AA.
 ID Q8BMZ3
 AC Q8BMZ3 ;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Tafazzin homolog.
 GN TAZ OR 913012G04R1K.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 MEDLINE=22354633; PubMed=12466851;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 Nature 420:1563-573 (2002)."
 RL 60,770 full-length cDNAs.";
 DR AK004035; BAC25063.1; -
 DR MGI: MGI:109626; TA2.
 DR GO: GO:0008415; Fatty acid transferase activity; IEA.
 DR GO: GO:0008152; Pyrometabolism; IEA.
 DR InterPro; IPR002123; Acyltransferase.
 DR InterPro; IPR000872; Tafazzin.
 DR Pfam; PF01553; Acyltransferase; 1.
 DR PRINTS; PR000979; TAFAZZIN.
 DR SMART; SM00563; P1sc; 1.
 SQ SEQUENCE 189 AA; 21863 MW; 123BCACAA40B78BFC CRC64;

Query Match Score 35; DB 11; Length 189;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 122 CRGDC 126

[1] RN RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv; NIPPONbare;
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 Overton T.L., Tsitran T., Kim M.M., Bera J.J., Jin S.S.,
 Fadros D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,
 Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
 Yang Q.Q., Haas B.B., Suh J.J., Quackenbush J.,
 White O., Salzberg S.L., Fraser C.M.,
 RT "Oryza sativa chromosome 3 BAC OSJNBA0042109 genomic sequence.";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 EMBL: AC104487; AA041141.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 218 AA; 24562 MW; 4PE0A501A4A17507 CRC64;

Query Match Score 35; DB 10; Length 218;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 203 CRGDC 207

RESULT 9
 Q8JU35 PRELIMINARY; PRT; 279 AA.
 ID Q8JU35
 AC Q8JU35;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Virus PhiChi1.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 OX NCBI_TaxID=114777;

RN RN
 RP SEQUENCE FROM N.A.
 MEDLINE=20177831; PubMed=10712697;
 RA Baranyi U., Klein R., Dubitz W., Kruger D.H., Witte A.;
 RT "The archaeal halophilic virus-encoded Dam-like methyltransferase M.
 phiChi1-I methylates adenine residues and complements dam mutants in
 the low salt environment of Escherichia coli.";
 Mol. Microbiol. 35:1168-1179(2000).

RN RN
 RP SEQUENCE FROM N.A.
 RX RX
 RA Klein R., Greineder B., Baranyi U., Witte A.;
 RT "The structural protein B of the archaeal virus phiChi1: evidence for
 processing in Natrialba magadii during virus maturation.";
 RL Virology 276:376-387(2000).

RN RN
 RP SEQUENCE FROM N.A.
 MEDLINE=20497008; PubMed=11040128;
 RA Klein R., Greineder B., Baranyi U., Witte A.;
 RT "The structural protein B of the archaeal virus phiChi1: evidence for
 processing in Natrialba magadii during virus maturation.";
 RL Virology 276:376-387(2000).

RN RN
 RP SEQUENCE FROM N.A.
 MEDLINE=22136043; PubMed=12139629;
 RA Klein R., Baranyi U., Rossler N., Greineder B., Scholz H., Witte A.;
 RT "Sequence analysis of the temperate virus PhiChi1 infecting the
 haloalkaliphilic archaeon Natrialba magadii.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: AF406305; ARM88605.1; -
 InterPro; IPR03615; RNR_nuc.
 InterPro; IPR007087; Znf_C2H2.
 Pfam; PF00096; zf-C2H2.
 SMART; SM00507; RNNHC_1.
 PROSITE; PS00028; ZINC_FINGER_CSH2_1.
 DR PROSITE; PS50157; ZINC_FINGER_CSH2_2.
 KW Hypothetical protein; Metal-binding; Zinc-finger.
 SQ SEQUENCE 279 AA; 31698 MW; 2A47BFE882306E13 CRC64;

RESULT 8
 Q85IN3 PRELIMINARY; PRT; 218 AA.
 ID Q85IN3
 AC Q85IN3 ;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OSJNBA0042109.11.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophytina; Embryophyta; Tracheophyta;
 OC Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartioideae; Oryzeae; Oryzae.
 NCBI_TaxID=39947;

092517
 ID 092517; PRELIMINARY; PRT; 118 AA.
 AC 092517;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Second triple gene block gene.
 OS Beet virus Q.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=71972;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98178056; PubMed=97114254;
 RA Koenig R., Pleij C., Beier C., Commandeur U.;
 RT "Genome properties of beet virus Q, a new furo-like virus from
 sugarbeet, determined from unpurified virus.";
 RL J. Gen. Virol. 79:2027-2036 (1998).
 DR EMBL; AJ221598; CAI1463_1;
 InterPro: IPR001896; Plant_vir_prot.
 Pfam: PF01307; Plant_vir_prot_1.
 ProDom: PD001561; Plant_vir_prot_1.
 Sequence: 118 AA; 12719 MW; A55ER6BC198123EB CRC64;

Query Match Score 35; DB 12; Length 118;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 109 CRGDC 113

RESULT 3
 Q9YPH2 PRELIMINARY; PRT; 118 AA.
 AC Q9YPH2;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Triple-gene-block second protein.
 OS Broad bean necrosis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=79918;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98190102; PubMed=9722878;
 RA Lu X., Yamamoto S., Tanaka M., Hibi T., Namba S.;
 RT "The genome organization of the broad bean necrosis virus (BBNV).";
 RL Arch. Virol. 143:1335-1348(1998).
 DR EMBL; D86638; BAA34697_1;
 InterPro: IPR01896; Plant_vir_prot.
 Pfam: PF01307; Plant_vir_prot_1.
 ProDom: PD001561; Plant_vir_prot_1.
 Sequence: 118 AA; 13255 MW; F7EC57D303FDSDA CRC64;

Query Match Score 35; DB 12; Length 118;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 110 CRGDC 114

RESULT 4
 Q9IV53 PRELIMINARY; PRT; 119 AA.
 AC Q9IV53;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Triple-gene-block protein 2.
 GN TGPB2.

OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=54-15;

092517
 ID 092517; PRELIMINARY; PRT; 118 AA.
 AC 092517;
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE Second triple gene block gene.
 OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Swedish.

RA Saverkov E.I., Sandgren M., Germundsson A.;
 RT "Complete sequence of RNA2 from potato mop-top virus (PMTV-Sw)." ;
 RL Submitted (MAY 2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ277556; CAB91102_1;
 DR InterPro; IPR01896; Plant_vir_prot.
 DR Pfam: PF01307; Plant_vir_prot_1.
 DR ProDom: PD001561; Plant_vir_prot_1.
 SQ SEQUENCE 119 AA; 13123 MW; CP15C8BC03305932 CRC64;

Query Match Score 35; DB 12; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 109 CRGDC 113

RESULT 5
 Q85292 PRELIMINARY; PRT; 119 AA.
 AC Q85292;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=37128;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Todd;
 RX MEDLINE=9508602; PubMed=7996148;
 RA Scott K.P., Kashiwaki S., Reavy B., Harrison B.D.;
 RT "The nucleotide sequence and potato mop-top virus RNA 2: a novel type
 of genome organization for a furovirus.";
 RT J. Gen. Virol. 75:3561-3568 (1994).
 DR EMBL; D30753; BAA06413_1;
 DR InterPro; IPR01896; Plant_vir_prot.
 DR Pfam: PF01307; Plant_vir_prot_1.
 DR ProDom: PD001561; Plant_vir_prot_1.
 SQ SEQUENCE 119 AA; 13109 MW; CP136F869821BBC2 CRC64;

Query Match Score 35; DB 12; Length 119;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 109 CRGDC 113

RESULT 6
 Q80QA2 PRELIMINARY; PRT; 119 AA.
 AC Q80QA2;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-Oct-2003 (TREMBLrel. 25, Last annotation update)

OS Potato mop-top virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Pomovirus.
 NCBI_TaxID=37128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=54-15;

Result No.	Score	Query	Match	Length	DB	ID	Description	
1	35	100.0	88	12	Q88801		Q88801 eastern equi	
2	35	100.0	118	12	O92517		O92517 beet virus	
3	35	100.0	118	12	O9YPH2		O9YPH2 broad bean	
4	35	100.0	119	12	Q9IV53		Q9IV53 potato	
5	35	100.0	119	12	Q85292		Q85292 potato	
6	35	100.0	119	12	Q800Q2		Q800Q2 potato	
7	35	100.0	189	11	Q8BM23		Q8BM23 mus musculus	
8	35	100.0	218	10	Q851N3		Q851N3 oryza sativa	
9	35	100.0	279	12	O8JL35		O8JL35 virus phich	
10	35	100.0	335	12	O8VA50		Q8VA50 ag80-663 vi	
11	35	100.0	336	4	O8NCQ7		Q8ncq7 homo sapiens	
12	35	100.0	353	11	O9CW26		O9CW26 mus musculus	
13	35	100.0	474	2	O84DX6		O84dx6 tropomyosin	
14	35	100.0	474	16	O83HY0		O83hy0 tropomyosin	
15	35	100.0	477	16	Q83G91		Q83g91 tropomyosin	
16	35	100.0	546	12	Q801B8		Q801b8 influenza a	
17	35	100.0	549	12	Q80IA8		Q80ia8 influenza a	
			18	35	Q80IC9		Q80ic9 influenza a	
			19	35	Q80Ics5		Q80ics5 influenza a	
			20	35	Q80IB9		Q80ib9 influenza a	
			21	35	Q80IB7		Q80ib7 influenza a	
			22	35	Q80IA1		Q80ia1 influenza a	
			23	35	Q80I97		Q80i97 influenza a	
			24	35	Q80I95		Q80i95 influenza a	
			25	35	Q80I82		Q80i82 influenza a	
			26	35	Q8E7Q7		Q8e7q7 influenza a	
			27	35	Q7T193		Q7t193 pagrus major	
			28	35	Q9YGC8		Q9ycg8 caenorhabditis	
			29	35	Q9YKC6		Q9yk6 venezuelan	
			30	35	Q9WC27		Q9wc27 salmon trout	
			31	32	Q8AYF9		Q8ayf9 salmon trout	
			32	32	Q88815		Q88815 eastern equi	
			33	32	Q88810		Q88810 eastern equi	
			34	32	Q88803		Q88803 eastern equi	
			35	32	Q88816		Q88816 eastern equi	
			36	32	Q88811		Q88811 eastern equi	
			37	32	Q88817		Q88817 eastern equi	
			38	32	Q88809		Q88809 eastern equi	
			39	32	Q88823		Q88823 eastern equi	
			40	32	Q88808		Q88808 eastern equi	
			41	32	Q88818		Q88818 eastern equi	
			42	32	Q88821		Q88821 eastern equi	
			43	32	Q88807		Q88807 eastern equi	
			44	32	Q88804		Q88804 eastern equi	
			45	32	Q88822		Q88822 eastern equi	
							ALIGNMENTS	
					Q88801	PRELIMINARY;	PRT;	BB AA.
					ID Q88801;			
					AC Q88801;	(TREMBLrel. 01, Created)		
					DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
					DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
					DB EI protein (Fragment).			
					OS Eastern equine encephalomyelitis virus.			
					OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae; OC Alphavirus.			
					OC Alpha virus.			
					NCBI_TaxID=11021;			
					RN [1]			
					RP SEQUENCE FROM N.A.			
					RC STRAIN=N-10365;			
					RX MEDLINE=94076404; PubMed=8254725;			
					RA Weaver S.C., Hagenbaugh A., Bellieu L.A., Gousset L., Mallampalli V.,			
					RA Holland J.J., Scott T.W.			
					RT "Evolution of alphaviruses in the eastern equine encephalomyelitis complex";			
					RT complex";			
					RL J. Virol. 68:158-169(1994).			
					DR EMBL; U01577; AAC53764.1;			
					DR InterPro; IPR002548; Alpha_E1_glycop.			
					DR InterPro; IPR007110; Ig-like.			
					DR Pfam; PP01589; Alpha_E1_glycop; 1.			
					FT NON_TER 1			
					SEQUENCE 88 AA; 9540 MW; CBB34D04C62C196F CRC64;			
					Query Match 100.0%; Score 35; DB 12; Length 88;			
					Best Local Similarity 100.0%; Pred. No. 9 6;			
					Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
					Qy 1 CRGDC 5			
					Db 24 CRGDC 28			
					RESULT 2			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

FT CHAIN 757 812 6 kDa PEPTIDE.
 FT CHAIN 813 1254 SPIKE GLYCOPROTEIN E1.
 FT ACT SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT SITE 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 701 721 POTENTIAL.
 FT TRANSMEM 794 813 POTENTIAL.
 FT TRANSMEM 1231 1248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138337 MW; 29DDEF3/F9E92C4B CRC64;

Query Match Score 91.4%; Best Local Similarity 80.0%; Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5 :||| Db 1188 CRGDC 1192

RESULT 15
 ID P0LS_EEVVM_ STANDARD; PRT; 1254 AA.
 AC Q66587; Q66589; Q66590; Q66591;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spike glycoprotein E1; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein E1].
 DE Venezuelan equine encephalitis virus (strain Mena II).
 OS Viruses;
 OC ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 NCBI TaxID=36384;
 RN 11

RP SEQUENCE FROM N.A.
 RX MEDLINE=93187617; PubMed=8445371;
 RA Sneider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.;
 RT "Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB viruses are not evolutionary derivatives of enzootic VEE subtype I-E or II viruses";
 RT Subgen. Virol. 74:519-523 (1993).
 CC -I- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -I- PBM: Specific enzymatic cleavages in vivo yield mature proteins.
 CC -I- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
 CC -I- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.

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CC DR EMBL; L04599; AAA42990_1; ALT TERM.
 DR EMBL; L04599; AAA42999_1; ALT SEQ.
 DR EMBL; L04599; AAA42992_1; ALT SEQ.
 DR EMBL; L04599; AAA42993_1; ALT SEQ.
 DR PIR; JO1979; JO1979.
 DR HSSP; P03315; IIVCP.

CC DR M6OPS; S03_001; -

CC DR InterPro; IPR002548; Alpha_E1_glycop.
 CC DR InterPro; IPR000936; Alpha_E2_glycop.
 CC DR InterPro; IPR002533; Alpha_E3_glycop.

DR InterPro; IPR009003; Cys_Ser trypsin.
 DR InterPro; IPR003336; Pla1_glycoprotE.
 DR InterPro; IPR07110; Ig-like.
 DR InterPro; IPR00930; Peptidase_S3.
 DR pfam; PF00944; Alpha core; 1.
 DR pfam; PF01589; Alpha_E1_glycop; 1.
 DR pfam; PF00943; Alpha_E2_glycop; 1.
 DR pfam; PF01563; Alpha_E3_glycop; 1.
 DR PRINTS; PRO0798; TOGAVIRIN.
 KW Coat protein; Polypeptide; Glycoprotein; Glycoprotein; Hydrolase;
 KW Serine protease.
 KW Serine protease.

DR COAT PROTEIN C.
 DR SPIKE GLYCOPROTEIN E3.
 DR SPIKE GLYCOPROTEIN E2.
 DR 6 kDa PEPTIDE.

DR SPIKE GLYCOPROTEIN E1.

DR CHARGE RELAY SYSTEM (BY SIMILARITY).

RESULT 13

Q	P	Query Match 91.4%; Best Local Matches 4;	Score 32; Pred. No. 1.1e+02;	Similari ty 80.0%; Mismatches 1;	STANDARD; PRT; 1254 AA.
POLs_EEVVB	POLs_EEVVB	POLs_EEVVB	POLs_EEVVB	POLs_EEVVB	POLs_EEVVB
P05674;	P05674;	P05674;	P05674;	P05674;	P05674;
C	C	C	C	C	C
T	T	T	T	T	T
01-NOV-1988 (Rel. 09, Created)	01-NOV-1988 (Rel. 09, Last sequence update)	16-OCT-2001 (Rel. 40, Last annotation update)	Structural polyprotein (P130) [Contains: Coat protein C (EC 3.4.21.-.)	(Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein E1].	Venezuelan equine encephalitis virus (strain TC-83).
[1]	[1]	[1]	[1]	[1]	[1]
Alphavirus.	Alphavirus.	Alphavirus.	Alphavirus.	Alphavirus.	Alphavirus.
NCBI_TaxID:11037;	NCBI_TaxID:11037;	NCBI_TaxID:11037;	NCBI_TaxID:11037;	NCBI_TaxID:11037;	NCBI_TaxID:11037;
SEQUENCE FROM N.A. PubMed=3755750;	SEQUENCE FROM N.A. PubMed=3755750;	SEQUENCE FROM N.A. PubMed=3755750;	SEQUENCE FROM N.A. PubMed=3755750;	SEQUENCE FROM N.A. PubMed=3755750;	SEQUENCE FROM N.A. PubMed=3755750;
LINEAR	LINEAR	LINEAR	LINEAR	LINEAR	LINEAR
Johnson B.J.B., Kinney R.M., Kost C.L., Trent D.W.;	"Molecular determinants of alphavirus neurovirulence: nucleotide and deduced protein sequence changes during attenuation of Venezuelan encephalitis virus";	J. Gen. Virol. 67:1951-1960 (1986).	J. Gen. Virol. 67:1951-1960 (1986).	J. Gen. Virol. 67:1951-1960 (1986).	J. Gen. Virol. 67:1951-1960 (1986).
-!- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.	-!- MISCELLANEOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.	-!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.	-!- SIMILARITY: THE PROTEASE IS PROBABLY PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB-SIB.CH/ANNOUNCE/ OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).	-!- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.	-!- MISCELLANEOUS: THE 6 KDA POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
CC	CC	CC	CC	CC	CC
EMBL; X04368; CAA27883.1; -.	PIR; A27871; VHIVVE.	HSSP; P03315; IVCP.	MBIOPS; S03_001; -.	INTERPRO; IPR002548; Alpha_E1_glycop.	INTERPRO; IPR000936; Alpha_E1_glycop.
INTERPRO; IPR002548; Alpha_E1_glycop.	INTERPRO; IPR000936; Alpha_E2_glycop.	INTERPRO; IPR002533; Alpha_E3_glycop.	INTERPRO; IPR009003; Cys_Ser_trypsin.	INTERPRO; IPR000336; Flavi_glycoprote.	INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR000930; Peptidase_S3.	PFAM; PF00344; Alpha_core; 1.	PFAM; PF00943; Alpha_E1_glycop; 1.	INTERPRO; IPR002533; Alpha_E3_glycop.	INTERPRO; IPR00336; Flavi_glycoprote.	INTERPRO; IPR007110; Ig-like.
INTERPRO; IPR000930; Peptidase_S3.	PFAM; PF00943; Alpha_E2_glycop; 1.	PFAM; PF01563; Alpha_B3_glycop; 1.	INTERPRO; IPR009003; Cys_Ser_trypsin.	INTERPRO; IPR00930; Peptidase_S3.	INTERPRO; IPR007110; Ig-like.
PRINTS; PRO0798; TOGAVIRIN.	PRINTS; PRO0798; TOGAVIRIN.	PRINTS; PRO0798; TOGAVIRIN.	PFAM; PF00944; Alpha_core; 1.	PFAM; PF01589; Alpha_E1_glycop; 1.	PFAM; PF00943; Alpha_E2_glycop; 1.
Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; Serine protease.	Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; Serine protease.	Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase; Serine protease.	PFAM; PF01563; Alpha_E3_glycop; 1.	PFAM; PF00943; Alpha_E2_glycop; 1.	PFAM; PF01563; Alpha_E3_glycop; 1.
CHAIN 1 275 SPIKE GLYCOPROTEIN E3.	CHAIN 1 275 SPIKE GLYCOPROTEIN E3.	CHAIN 1 275 SPIKE GLYCOPROTEIN E3.	DR InterPro; IPR002548; Alpha_E1_glycop.	DR InterPro; IPR002548; Alpha_E1_glycop.	DR InterPro; IPR002548; Alpha_E1_glycop.
CHAIN 276 334 SPIKE GLYCOPROTEIN E2.	CHAIN 276 334 SPIKE GLYCOPROTEIN E2.	CHAIN 276 334 SPIKE GLYCOPROTEIN E2.	DR InterPro; IPR000936; Alpha_E2_glycop.	DR InterPro; IPR000936; Alpha_E2_glycop.	DR InterPro; IPR000936; Alpha_E2_glycop.
CHAIN 335 757 6 kDa PEPTIDE.	CHAIN 335 757 6 kDa PEPTIDE.	CHAIN 335 757 6 kDa PEPTIDE.	DR InterPro; IPR02533; Alpha_E3_glycop.	DR InterPro; IPR02533; Alpha_E3_glycop.	DR InterPro; IPR02533; Alpha_E3_glycop.
CHAIN 758 812 SPIKE GLYCOPROTEIN E1.	CHAIN 758 812 SPIKE GLYCOPROTEIN E1.	CHAIN 758 812 SPIKE GLYCOPROTEIN E1.	DR InterPro; IPR009003; Cys_Ser_trypsin.	DR InterPro; IPR009003; Cys_Ser_trypsin.	DR InterPro; IPR009003; Cys_Ser_trypsin.
CHAIN 813 1254 CHARGE RELAY SYSTEM (BY SIMILARITY).	CHAIN 813 1254 CHARGE RELAY SYSTEM (BY SIMILARITY).	CHAIN 813 1254 CHARGE RELAY SYSTEM (BY SIMILARITY).	DR InterPro; IPR00336; Flavi_glycoprote.	DR InterPro; IPR00336; Flavi_glycoprote.	DR InterPro; IPR00336; Flavi_glycoprote.
ACT SITE 152 152 CHARGE RELAY SYSTEM (BY SIMILARITY).	ACT SITE 152 152 CHARGE RELAY SYSTEM (BY SIMILARITY).	ACT SITE 152 152 CHARGE RELAY SYSTEM (BY SIMILARITY).	DR InterPro; IPR01110; Ig-like.	DR InterPro; IPR01110; Ig-like.	DR InterPro; IPR01110; Ig-like.
ACT SITE 158 158 CHARGE RELAY SYSTEM (BY SIMILARITY).	ACT SITE 158 158 CHARGE RELAY SYSTEM (BY SIMILARITY).	ACT SITE 158 158 CHARGE RELAY SYSTEM (BY SIMILARITY).	DR InterPro; IPR00930; Peptidase_S3.	DR InterPro; IPR00930; Peptidase_S3.	DR InterPro; IPR00930; Peptidase_S3.
TRANSHEM 226 226 POTENTIAL.	TRANSHEM 226 226 POTENTIAL.	TRANSHEM 226 226 POTENTIAL.	PFAM; PF01589; Alpha_core; 1.	PFAM; PF01589; Alpha_core; 1.	PFAM; PF01589; Alpha_core; 1.
TRANSHEM 702 718 POTENTIAL.	TRANSHEM 702 718 POTENTIAL.	TRANSHEM 702 718 POTENTIAL.	DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.
TRANSHEM 792 808 POTENTIAL.	TRANSHEM 792 808 POTENTIAL.	TRANSHEM 792 808 POTENTIAL.	DR InterPro; IPR00930; Peptidase_S3.	DR InterPro; IPR00930; Peptidase_S3.	DR InterPro; IPR00930; Peptidase_S3.
TRANSHEM 1231 1247 POTENTIAL.	TRANSHEM 1231 1247 POTENTIAL.	TRANSHEM 1231 1247 POTENTIAL.	DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.
CARBONYD 286 286 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 286 286 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 286 286 N-LINKED (GLCNAC, .) (POTENTIAL).	KW	KW	KW
CARBONYD 546 546 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 546 546 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 546 546 N-LINKED (GLCNAC, .) (POTENTIAL).	FT	FT	FT
CARBONYD 652 652 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 652 652 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 652 652 N-LINKED (GLCNAC, .) (POTENTIAL).	CHAIN	CHAIN	CHAIN
CARBONYD 946 946 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 946 946 N-LINKED (GLCNAC, .) (POTENTIAL).	CARBONYD 946 946 N-LINKED (GLCNAC, .) (POTENTIAL).	FT	FT	FT
SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	COAT PROTEIN C.	COAT PROTEIN C.	COAT PROTEIN C.
SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	SEQUENCE 1254 AA; MW: 138485 SPIKE GLYCOPROTEIN B3.	COAT PROTEIN; Hydrolase; Glycoprotein; Transmembrane; Glycoprotein; Hydrolase.	COAT PROTEIN; Hydrolase; Glycoprotein; Transmembrane; Glycoprotein; Hydrolase.	COAT PROTEIN; Hydrolase; Glycoprotein; Transmembrane; Glycoprotein; Hydrolase.

RESULT 10
TRE2_SALSA
 ID TRF2_SALSA
 STANDARD; PRT; 691 AA.
 Qy 1 CRGDC 5
 Sq 185 CKGDC 189
 Db 185 CKGDC 189
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 MEDLINE=94122797; PubMed=8293074;
 RA Kvinesdal A.M.; Roervik K.A.; Alestrem P.;
 RT "Cloning and characterization of Atlantic salmon (*Salmo salar*) serum
 transferin cDNA."
 OC Mol. Mar. Biol. Biotechnol. 2:233-238 (1993).
 OX [1]
 RN [2]
 RP SEQUENCE OF 19-37.
 RC TISSUE=Serum;
 RA Roed K.H.; Dahl A.K.; Flengsrud R.; Midthjell L.; Roervik K.A.;
 RT "Immunobioassay and partial characterization of serum transferrin from
 Atlantic salmon (*Salmo salar* L.)."
 RL Fish Shallow Immuno. 5:71-80 (1995)
 CC -I- FUNCTION: Transferrins are iron binding transport proteins which
 can bind two atoms of ferric iron in association with the binding
 of an anion, usually bicarbonate. It is responsible for the
 transport of iron from sites of absorption and heme degradation to
 those of storage and utilization. Serum transferrin may also have
 a further role in stimulating cell proliferation.
 CC -I- SUBUNIT: Monomer.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Abundant in liver and serum with smaller
 amounts found in the stomach and kidney.
 CC -I- DOMAIN: Composed of two homologous domains.
 CC -I- SIMILARITY: Belongs to the transferrin family.
 DR HSSP; P5610; IAOV.
 DR InterPro; IPR01156; Transferrin.
 DR Pfam; PF00405; transferrin_2.
 DR PRINTS; PR00422; TRANSFERRIN_1.

RESULT 11
POLS_EEEV
 ID POLS_EEEV
 STANDARD; PRT; 1239 AA.
 AC P07678;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural Polypeptide (P130) [Contains: Coat protein C (EC 3.4.21.-);
 DE (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2;
 DE 6 kDa peptide; Spike glycoprotein E1].
 OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis
 virus).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX [1] - NCBI_TaxID=11021;
 RN SEQDB=82V-2137;
 RP STRAIN=82V-2137;
 RC MEDLINE=87292265; PubMed=28886548;
 RA Chang G.-J.U., Trent D.W.;

CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation to
 CC those of storage and utilization. Serum transferrin may also have
 CC a further role in stimulating cell proliferation.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Abundant in liver and serum with smaller
 CC amounts found in the stomach and kidney.

CC -!- DOMAIN: Composed of two homologous domains.

CC -!- SIMILARITY: Belongs to the transferrin family.

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 CC or send an email to license@isb-sib.ch).

CC DR EMBL; L20313; AAA18838; 1; - .

CC DR EMBL; L26909; ARCA221.1; - .

CC DR PIR; I51350; .

CC DR HSSP; P56410; IAOV.

CC DR InterPro; IPR001156; Transferrin.

CC DR Pfam; PF00405; transferrin; 2.

CC DR PRINTS; PRO0422; TRANSFERRIN.

CC SMART; SM0094; TR_FER; 2.

CC DR PROSITE; PS00205; TRANSFERIN_1; 2.

CC DR PROSITE; PS00206; TRANSFERIN_-; 2.

CC DR PROSITE; PS00207; TRANSFERIN_3; 1.

CC KW Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;

CC KW Signal.

FT SIGNAL 1 18 SEROTRANSFERRIN I.

FT CHAIN 19 690 BY SIMILARITY.

FT DISULPID 28 50 BY SIMILARITY.

FT DISULPID 127 207 BY SIMILARITY.

FT DISULPID 172 186 BY SIMILARITY.

FT DISULPID 235 249 BY SIMILARITY.

FT DISULPID 343 379 BY SIMILARITY.

FT DISULPID 353 370 BY SIMILARITY.

FT DISULPID 404 681 BY SIMILARITY.

FT DISULPID 419 642 BY SIMILARITY.

FT DISULPID 451 529 BY SIMILARITY.

FT DISULPID 475 670 BY SIMILARITY.

FT DISULPID 485 499 BY SIMILARITY.

FT DISULPID 496 512 BY SIMILARITY.

FT DISULPID 569 583 BY SIMILARITY.

FT METAL 74 704 IRON 1 (BY SIMILARITY).

FT METAL 104 104 IRON 1 (BY SIMILARITY).

FT METAL 201 201 IRON 1 (BY SIMILARITY).

FT METAL 257 257 IRON 1 (BY SIMILARITY).

FT METAL 394 394 IRON 2 (BY SIMILARITY).

FT METAL 428 428 IRON 2 (BY SIMILARITY).

FT METAL 523 523 IRON 2 (BY SIMILARITY).

FT METAL 591 591 IRON 2 (BY SIMILARITY).

FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).

FT BINDING 129 129 CARBONATE 1 (BY SIMILARITY).

FT BINDING 134 134 CARBONATE 1 (BY SIMILARITY).

FT BINDING 136 136 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).

FT BINDING 137 137 CARBONATE 1 (VIA AMIDE NITROGEN) (BY SIMILARITY).

FT BINDING 453 453 CARBONATE 2 (BY SIMILARITY).

FT BINDING 457 457 CARBONATE 2 (BY SIMILARITY).

FT BINDING 459 459 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).

FT BINDING 460 460 CARBONATE 2 (VIA AMIDE NITROGEN) (BY SIMILARITY).

FT CONFLICT 34 34 E > O (IN REF. 3).

SQ SEQUENCE 690 AA; 74597 MW; D1F4C74AGAFA3FB CRC64;

Best Local Similarity 80.0%; Pred. No. 64;
 Matches 4; Conservative 1; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 186 CRGDC 190

RESULT 9

ID TRFE_ORYLA STANDARD; PRT; 690 AA.

ID TRFE_ORYLA P79819; RP; SEQUENCE FROM N.A.

AC P79819; RX MEDLINE=96414927; PubMed=8817928;

DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Serotransferrin precursor (Medaka fish) (Japanese ricefish).

OS Orzyza latipes (Medaka fish).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryziidae.

OC OC NCBI_TaxID=8096;

OX OX [1];

RN RN [1]

RA Mikawa N., Hirano I., Aoki T.; RT "Structure of medaka transferrin gene and its 5'-flanking region." ; RL Mol. Mar. Biol. Biotechnol. 5:25-29 (1996).

CC -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DOMAIN: Composed of two homologous domains.

CC -!- SIMILARITY: Belongs to the transferrin family.

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CC -!- DOMAIN: Composed of two homologous domains.

CC -!- SIMILARITY: Belongs to the transferrin family.

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DR EMBL; D64033; PAA10901.1; - .

DR HSSP; P56410; IAOV.

DR InterPro; IPR001156; Transferrin.

DR Pfam; PF00405; transferrin; 2.

DR PRINTS; PR00422; TRANSFERRIN.

DR SMART; SM00094; TR_FER; 2.

DR PROSITE; PS00205; TRANSFERRIN_1; 2.

DR PROSITE; PS00206; TRANSFERRIN_2; 2.

DR PROSITE; PS00207; TRANSFERRIN_3; FALSE NEG.

DR Transport; Iron transport; Glycoprotein; Metal-binding Repeat;

KW KW Signal.

FT SIGNAL 1 17 BY SIMILARITY.

FT CHAIN 18 690 BY SIMILARITY.

FT DISUFID 27 49 BY SIMILARITY.

FT DISUFID 126 206 BY SIMILARITY.

FT DISUFID 171 185 BY SIMILARITY.

FT DISUFID 234 248 BY SIMILARITY.

FT DISUFID 343 379 BY SIMILARITY.

FT DISUFID 353 370 BY SIMILARITY.

FT DISUFID 404 404 BY SIMILARITY.

FT DISUFID 419 643 BY SIMILARITY.

FT DISUFID 452 530 BY SIMILARITY.

FT DISUFID 476 671 BY SIMILARITY.

FT DISUFID 486 499 BY SIMILARITY.

FT DISUFID 496 513 BY SIMILARITY.

FT DISUFID 570 584 BY SIMILARITY.

FT METAL 73 73 IRON 1 (BY SIMILARITY).

FT METAL 103 103 IRON 1 (BY SIMILARITY).

FT METAL 200 200 IRON 1 (BY SIMILARITY).

Query Match 91.4%; Score 32; DB 1; Length 690;

modified and this statement is not removed.; Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; AAC04500; AAC0450_1; -.
 CC DR HSSP; P12643; 3BMP.
 CC DR InterPro; IPR002405; Inhibin_alpha.
 CC DR InterPro; IPR001839; TGFb.
 CC DR Pfam; PF00019; TGF-beta; 1.
 CC DR PRINTS; PRO0669; INHIBINA.
 CC DR ProDom; PD000357; TGFb; 1.
 CC DR SMART; SMO0204; TGFb; 1.
 CC DR PROSITE; PS00250; TG-BETA1; 1.
 CC KW Growth factor; Cytokine; Glycoprotein; Signal.

FT SIGNAL 1 27 POTENTIAL.
 FT PROPEP 28 319 POTENTIAL.
 FT CHAIN 320 454 GROWTH/DIFFERENTIATION FACTOR 9 .
 FT DISULFID 323 419 BY SIMILARITY.
 FT DISULFID 382 451 BY SIMILARITY.
 FT CARBOHYD 386 453 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 454 AA; 51443 MW; 94EA366890CDB27 CRC64 ;

Query Match 91.4%; Score 32; DB 1; Length 454;
 Best Local Similarity 80.0%; Pred. No. 61;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

Qy 1 CRGDC 5 :|||
 Db 382 CRGDC 386 STANDARD; PRT; 690 AA.

RESULT 7

BGLX_ERWCH ID _BGLX_ERWCH STANDARD; PRT; 654 AA.
 AC Q46634;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Periplasmic beta-D-glucosidase/beta-D-xyllosidase precursor [Includes: Beta glucosidase [EC 3.2.1.21] (Gentiothiobase) (Celllobiase); Beta-D-xyllosidase [EC 3.2.1.37] (1,4-beta-D-xylan xylohydrolyase) (Xylan 1,4-beta-D-xylosidase)].
 GN BGXA.
 OS *Bacillus* chrysanthemi.

OC Enterobacteriaceae; Pectobacterium; Enterobacteriales;
 OX NCBI_TAXID=556;
 RN SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP STRAIN=D1;

RC MEDLINE=95198684; PubMed=7891660;

RA Vroemen S., Heijnen J.J., Boyd C., Henriëtta B., Keen N.T.;
 RT "Cloning and characterization of the 5' region of the Atlantic salmon (*Salmo* salar) transferrin-encoding gene.";

RL Mol. Gen. Genet. 246:465-477(1995).

CC ACTIVITIES.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing beta-D-glucose residues with release of beta-D-glucans.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-xylans so as to remove successive D-xylene residues from the non-reducing termini.
 CC -!- SUBCELLULAR LOCATION: Periplasmic.

CC -!- SIMILARITY: Belongs to family 3 of glycosyl hydrolases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL; U08606; AAA80156; DR InterPro; IPR002772; Glyco_hydro_3C.
 CC DR InterPro; IPR001764; Glyco_hydro_3N.
 CC DR Pfam; PF01933; Glyco_hydro_3_C_1.
 CC DR PRINTS; PR00133; GLYHYDRASE3.
 CC DR PROSITE; PS0075; GLYCOSYL_HYDROL_F3; 1.
 CC KW Hydrolase; Glycosidase; Xyylan degradation; Periplasmic; Signal;
 CC KW Multifunctional enzyme.
 CC FT SIGNAL 1 25 POTENTIAL.
 CC FT CHAIN 26 654 PERIPLASMIC_BETA-GLUCOSIDASE/BETA-XYLOSIDASE.
 CC FT ACT_SITE 235 BY SIMILARITY.
 CC FT ACT_SITE 360 BY SIMILARITY.
 CC SQ SEQUENCE 654 AA; 71584 MW; 5CDEFEE2162A7A95 CRC64 ;
 CC Query Match 91.4%; Score 32; DB 1; Length 654;
 CC Best Local Similarity 80.0%; Pred. No. 61;
 CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 CRGDC 5 :|||
 CC Db 367 CRGDC 371

CC RESULT 8

TRFL_SALSA STANDARD; PRT; 690 AA.

ID TRFL_SALSA P80426;
 AC 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Serotransferrin I precursor (Sliderophilin I) (STF I).
 STF1.
 GN Salmo salar (Atlantic salmon).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

NCBI_TaxID=8030;

RN [1] -

SEQUENCE FROM N.A.

RC TISSUE=liver
 RX MEDLINE=95122797; PubMed=8293074;

RA Kvindingdal A.M.; Roervik K.A.; Alestroem P.;

RT "Cloning and characterization of Atlantic salmon (*Salmo* salar) serum

RT transferrin cDNA";

RT Mol. Mar. Biol. Biotechnol. 2:233-238(1993).

RL [2]

SEQUENCE OF 1-64 FROM N.A.

RP MEDLINE=95121925; PubMed=821802;

RA Kvindingdal A.M.;

RT "Characterization of the 5' region of the Atlantic salmon (*Salmo* salar) serum transferrin from the binding protein from the serum of Atlantic salmon (*Salmo* salar L.)";

RT Fish Shellfish Immunol. 5:71-80(1995).

-!- FUNCTION: Transferrins are iron binding transport proteins which can bind two atoms of ferric iron in association with the binding

factor-beta superfamily containing a novel pattern of cysteines.";
 RT J. Biol. Chem. 268:3444-3449(1993).
 RL -|- FUNCTION: REQUIRED FOR OVARIAN FOLLICULogenesis.
 CC -|- SUBUNIT: HOMODIMER OR HETEROdimer (POTENTIAL). BUT, IN CONTRAST TO
 OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED.
 CC -|- TISSUE SPECIFICITY: Ovary.
 CC -|- SIMILARITY: Belongs to the TGF-beta family.

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 CC EMBL; L06444; AAA53035.1; - .
 DR PIR; S45284; S45294.
 DR HSSP; P12643; 3BMP.
 DR PRINTS; PRO0669; INHIBINA.
 DR PRODOM; PDD00357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGFB_BETA_1; 1.
 DR PROSITE; PS00250; TGFB_BETA_1; 1.
 DR Growth factor; Cytokine; Glycoprotein; Signal.
 DR SIGNAL; 1 29 POTENTIAL.
 DR PROPEP; 30 306 POTENTIAL.
 DR CHAIN; 307 441 GROWTH/DIFFERENTIATION FACTOR 9.
 DR DISULFID; 340 406 BY SIMILARITY.
 DR DISULFID; 369 438 BY SIMILARITY.
 FT DISULFID; 373 440 BY SIMILARITY.
 FT CARBOHYD; 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD; 229 229 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD; 258 258 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD; 325 325 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 441 AA; 49636 MW; E27071359B99C3C CRC64;

Query Match 91.4%; Score 32; DB 1; Length 441;
 Best Local Similarity 80.0%; Pred. No. 42; RT
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 369 CRGDC 373

RESULT 6

GDF9_HUMAN STANDARD; PRT; 454 AA.
 ID GDF9_HUMAN STANDARD; PRT; 454 AA.
 AC 060353; AC 060353;
 DT 15-JUL-1999 (Rel. 38, Created) DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update) DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DB Growth/differentiation factor 9 precursor (GDF-9). DB Growth/differentiation factor 9 precursor (GDF-9).
 GN GDF9. GN GDF9.
 OS Homo sapiens (Human). OS Homo sapiens (Human).
 OC Mammalia; Eutheria; Chordata; Vertebrata; Butteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN NCBITaxID-9606; RN NCBITaxID-9606;
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.

RA Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,
 RA Davis C.A., Kader K., Miegel T., Pitluck S., Pollard M., Rojeski H.,
 RA Subramanian S., Martin C.H.; Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RL -|- FUNCTION: REQUIRED FOR OVARIAN FOLLICULogenesis. BUT, IN CONTRAST TO
 CC -|- SUBUNIT: HOMODIMER OR HETEROdimer (POTENTIAL). BUT, IN CONTRAST TO
 OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
 CC -|- SIMILARITY: Belongs to the TGF-beta family.

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CC OTHER MEMBERS OF THIS FAMILY, CANNOT BE DISULFIDE-LINKED (BY
 CC SIMILARITY: Belongs to the TGF-beta family.
 CC -|- SIMILARITY: It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; AF078545; AAC28089.2; - .
 DR HSSP; P12643; 3BMP.
 DR InterPro; IPR02405; Inhibin_alpha.
 DR InterPro; IPR01839; TGFB.
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PRO1669; INHIBINA.
 DR PRODOM; PD000357; TGFB; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00230; TGFB_BETA_1; 1.
 DR KW Growth factor; Cytokine; Glycoprotein; Signal.
 DR FT SIGNAL; 1 27 POTENTIAL.
 DR FT PROPEP; 28 318 POTENTIAL.
 DR FT CHAIN; 319 453 BY SIMILARITY.
 DR FT DISULFID; 352 418 BY SIMILARITY.
 DR FT DISULFID; 381 450 BY SIMILARITY.
 DR FT DISULFID; 385 452 BY SIMILARITY.
 DR FT CARBOHYD; 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 DR FT CARBOHYD; 236 236 N-LINKED (GLCNAC. .) (POTENTIAL).
 DR FT CARBOHYD; 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
 DR FT CARBOHYD; 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
 DR FT CARBOHYD; 337 337 N-LINKED (GLCNAC. .) (POTENTIAL).
 DR SQ SEQUENCE 453 AA; 51776 MW; 1911A66A/20E2B85 CRC64;

Query Match 91.4%; Score 32; DB 1; Length 453;
 Best Local Similarity 80.0%; Pred. No. 44;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 5

GDF9_HUMAN STANDARD; PRT; 454 AA.
 ID GDF9_HUMAN STANDARD; PRT; 454 AA.
 AC 077681; AC 077681;
 DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update) DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Growth/differentiation factor 9 precursor (GDF-9). DE Growth/differentiation factor 9 precursor (GDF-9).
 GN Ovis_aries (Sheep). GN Ovis_aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis. OC Bovidae; Caprinae; Ovis.
 RN NCBITaxID-9940; RN NCBITaxID-9940;
 RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A.
 RA Bodensteiner K.J., Clay C.M., Moeller C.L., Sawyer H.R.; MEDLINE=9915226; PubMed=9916005;
 RA "Molecular cloning of the ovine growth/differentiation factor-9 gene
 RT and expression of growth/differentiation factor-9 in ovine and bovine
 RT ovaries."; Biol. Reprod. 60:381-386(1999).
 CC -|- FUNCTION: REQUIRED FOR OVARIAN FOLLICULogenesis.
 CC -|- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL). BUT, IN CONTRAST TO
 CC use by non-profit institutions as long as its content is in no way

RESULT 12
VHWEVE
 structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
 N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
 C;Species: eastern equine encephalomyelitis virus
 C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
 C;Accession: A28816
 R;Chang, G.J.J.; Trent, D.W.
 J. Gen. Virol. 68, 2129-2142, 1987
 A;Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine
 A;Reference number: A28816; MUID: 87282265; PMID: 2886548
 A;Accession: A28816
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X05816; PIDN:CAA29261.1; PID:962075
 C;Superfamily: togavirus structural Polyprotein
 C;Keywords: coat protein; glycoprotein; transmembrane protein
 P;1-259/Product: coat protein C #status predicted <CP>
 P;261-277/Domain: membrane Glycoprotein E3 #status predicted <TM1>
 P;323-742/Product: membrane Glycoprotein E2 #status predicted <TM2>
 P;684-724/Domain: transmembrane #status predicted <TN2>
 P;727-737/Domain: transmembrane #status predicted <TN3>
 P;743-798/Product: 6K protein #status predicted <KP>
 P;799-1239/Domain: transmembrane #status predicted <TN4>
 P;1211-1235/Domain: transmembrane #status predicted <TN5>
 P;49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 91.4%; Score 32; DB 1; Length 1239;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1175 CKGDC 1179

RESULT 13
VHWEVE
 structural polyprotein - eastern equine encephalomyelitis virus (strain VA3[Ten Broeck])
 N;Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
 C;Species: eastern equine encephalomyelitis virus
 A;Note: host Equus caballus (domestic horse)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
 C;Accession: A39992
 R;Weaver, S.C.; Scott, T.W.; Rico-Hesse, R.
 Virology 182, 774-784, 1991
 A;Title: Molecular evolution of eastern equine encephalomyelitis virus in North America.
 A;Reference number: A39992; MUID: 91220727; PMID: 2024496
 A;Accession: A39992
 A;Molecule type: genomic RNA
 A;Residues: 1-1240 <WEA>
 A;Cross-references: GB:M63094; PIDN:AAA42980.1; PID:9323697
 A;Note: the authors translated the codon AGC for residue 836 as Arg and GUU for residue
 C;Superfamily: togavirus structural Polyprotein
 C;Keywords: coat protein; glycoprotein; transmembrane protein
 P;1-256/Product: coat protein C #status predicted <CP>
 P;259-276/Domain: transmembrane #status predicted <TM1>
 P;261-323/Product: membrane Glycoprotein E3 #status predicted <EG3>
 P;695-712/Domain: transmembrane #status predicted <TM2>
 P;722-738/Domain: transmembrane #status predicted <TM3>
 P;744-759/Product: 6K protein #status predicted <KP6>
 P;781-799/Domain: transmembrane #status predicted <TM4>
 P;800-1240/Product: membrane Glycoprotein E1 #status predicted <EG1>
 P;1236-1256/Domain: transmembrane #status predicted <TM5>
 P;49,271,625,638,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 91.4%; Score 32; DB 1; Length 1240;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
S26373
 genome polyprotein - eastern equine encephalomyelitis virus
 N;Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein E2; envelope
 C;Species: eastern equine encephalomyelitis virus
 C;Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 26-Aug-1999
 C;Accession: S26373
 R;Volchkov, V.E.; Volchkova, V.A.; Netsov, S.V.
 A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genome
 A;Reference number: S26369; MUID: 91375524; PMID:1896061
 A;Accession: S26373
 A;Molecule type: mRNA
 A;Residues: 1-1241 <WOL>
 A;Cross-references: EMBL:X63135; PIDN:CAA44845.1; PID:959186
 A;Note: sequence could not be checked because of bad print in paper
 C;Superfamily: togavirus structural Polyprotein
 C;Keywords: capsid protein; envelope protein; Glycoprotein; polyprotein
 P;1-260/Product: capsid protein C #status predicted <CP>
 P;261-323/Product: envelope protein E3 #status predicted <EP3>
 P;324-743/Product: envelope protein E2 #status predicted <EP2>
 P;744-800/Product: 6K protein #status predicted <KP>
 F;801-1241/Product: envelope protein E1 #status predicted <EP1>
 Query Match 91.4%; Score 32; DB 2; Length 1241;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1177 CKGDC 1180

RESULT 15
S72350
 structural polyprotein - eastern equine encephalomyelitis virus
 N;Contains: 6K protein; capsid protein; E1 protein; E2 protein; E3 protein
 C;Species: eastern equine encephalomyelitis virus
 C;Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 26-Aug-1999
 C;Accession: S72350
 R;Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Volchkov, V.E.; Chang, G.J.;
 Virology 197, 375-390, 1993
 A;Title: A comparison of the nucleotide sequences of eastern and western equine encephalomyelitis viruses
 A;Reference number: S72349; MUID: 94025587; PMID: 8105605
 A;Accession: S72350
 A;Status: preliminary
 A;Molecule type: genomic RNA
 A;Residues: 1-1242 <WEA>
 A;Cross-references: EMBL:U01034; PIDN: AAC53735.1; PID:g393008
 C;Superfamily: togavirus structural Polyprotein
 Query Match 91.4%; Score 32; DB 2; Length 1242;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 1178 CKGDC 1182

Search completed: September 22, 2004, 06:52:57
 Job time : 41 secs

hypothetical protein At4g09620 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 R;Anonymous: The European Union *Arabidopsis* Genome Sequencing Consortium, The Cold Spring
 Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
 A;Reference number: A85001; MUID:10617198;
 A;Accession: D85098
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-210 <STO>
 A;Cross-references: GB NC_001268; NID:97267657; PIDN:CAB78085.1; GSPDB:GN00140
 C;Genetics:
 A;Gene: At4g09620
 A;Map position: 4

RESULT 8
 S45284
 growth/differentiation factor GDF-9 precursor - mouse
 Query Match 91.4%; Score 32; DB 2; Length 210;
 Best Local Similarity 80.0%; Pred. No. 57;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CRGDC 5
 Db 195 CKGDC 199

RESULT 9
 S533805
 beta-glucosidase/xylosidase - *Erwinia chrysanthemi*
 C;Species: *Erwinia chrysanthemi*
 C;Date: 27-Oct-1995 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C;Accession: S533805
 R;Vorlemen, S.; Heldens, J.; Boyd, C.; Henriksat, B.; Keen, N.T.
 A;Title: Cloning and characterization of the bgxA gene from *Erwinia chrysanthemi* D1 whic

A;Reference number: S533805; MUID:95198684; PMID:7891660
 A;Accession: S533805
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-654 <VRO>
 Query Match 91.4%; Score 32; DB 2; Length 654;
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 367 CKGDC 371

RESULT 10
 T11749
 transferrin - Atlantic salmon
 C;Species: *Salmo salar* (Atlantic salmon)
 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C;Accession: T11749
 R;Kvingedal, A.M.; Rorvik, K.A.; Alestrom, P.
 Mol. Marine Biol. Biotechnol. 2, 233-238, 1993
 A;Title: Cloning and characterization of Atlantic salmon (*Salmo salar*) serum transferrin
 A;Reference number: Z17332; MUID:94122797; PMID:8293074
 A;Accession: T11749
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-690 <KV>
 A;Cross-references: EMBL:L20313; NID:9431609; PIDN:AAA18838.1; PID:g431610
 A;Experimental source: liver
 C;Superfamily: transferrin; transferrin repeat homology
 C;Keywords: iron binding

Query Match 91.4%; Score 32; DB 2; Length 690;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 186 CKGDC 190

RESULT 11
 C87789
 protein C34G6.6 (Imported) - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C;Accession: C87789
 R;Anonymous, The C. elegans Sequencing Consortium,
 Science 282, 1012-1018, 1998
 A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A;Reference number: A75000; MUID:99069613; PMID:9951916
 A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
 A;Accession: C87789
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1011 <STO>
 A;Cross-references: GB:chr_I; PIDN:AAB52479.1; PID:g1943841; GSPDB:GN00019; CESP:C34G6.6
 C;Genetics:
 A;Gene: C34G6.6
 A;Map position: 1

Query Match 91.4%; Score 32; DB 2; Length 1011;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 879 CKGDC 883

Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 301 CRGDC 305

RESULT 3

T26044 hypothetical protein W01C8.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26044
R;Nhan, M.
Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid W01C8.
A;Reference number: 220142
A;Accession: T26044
A;Status: preliminary; translated from GB/EMBL/DDBj
A;Molecule type: DNA
A;Residues: 1-1076 <NHA>
A;Cross-references: EMBL:U41508; PIDN:AAA82623.1; CESP:W01C8.3
C;Genetics:
A;Gene: CESP:W01C8.3
A;Introns: 59/3; 92/2; 157/3; 189/3; 220/2; 251/3; 275/2; 319/1; 374/3; 407/2
Query Match Score 35; DB 2; Length 1076;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 278 CRGDC 282

Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4

B45206 metallothionein 2 - *Caenorhabditis elegans*
N;Alternate names: metallothionein I
C;Species: *Caenorhabditis elegans*
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 29-Oct-1999
R;Freedman, J.H.; Slice, L.W.; Dixon, D.; Fire, A.; Rubin, C.S.
J. Biol. Chem. 268, 2554-2564, 1993
A;Title: The novel metallothionein genes of *Caenorhabditis elegans*. Structural organization
A;Reference number: A45206; MUID: 93155063; PMID: 8428932
A;Accession: B45206
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-75 PRE>
A;Note: Sequence extracted from NCBI backbone (NCBI:124147)
R;Imagawa, M.; Onozawa, T.; Okumura, K.; Osada, S.; Nishihara, T.; Kondo, M.
Biochem. J. 268, 237-240, 1990
A;Title: Characterization of metallothionein cDNAs induced by cadmium in the nematode *Caenorhabditis elegans*
A;Reference number: S09714; MUID: 90262552; PMID: 2344361
A;Accession: S09714
A;Molecule type: mRNA
A;Residues: 1-75 <INA>
A;Cross-references: EMBL:X53244; PIDN:g6779; PIDN:CAA37334.1; PID: g6780
A;Accession: T29721
A;Status: preliminary; translated from GB/EMBL/DDBj
A;Residues: 1-75
A;Molecule type: DNA
A;Residues: 1-75 <GRE>
A;Cross-references: EMBL:U64853; PIDN:AAB04979.1; GSPDB.GN00023; CESP:K11G9.6
C;Genetics:
A;Gene: CESP:K11G9.6
A;Map position: 5

RESULT 5

T48370 hypothetical protein F12E4.220 - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 28-Jul-2000
C;Accession: T48370
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Newes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24492
A;Accession: T48370
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <BSV>
A;Cross-references: EMBL:AL162751
A;Experimental source: cultivar Columbia; BAC clone F12E4
C;Genetics:
A;Map position: 5
A;Introns: 30/2; 76/3
A;Note: F12E4.220
C;Superfamily: *Arabidopsis thaliana* hypothetical protein F12E4.220

Query Match Score 32; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 40;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 127 CRGDC 131

RESULT 6

A48608 E1 glycoprotein - eastern equine encephalomyelitis virus (fragment)
C;Species: eastern equine encephalomyelitis virus
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1999 #text_change 26-Aug-1999
C;Accession: A48608
C;Weaver, S.C.; Bellilew, L.; Repik, P.M.; Scott, T.W.; Holland, J.J.
Virology 195, 700-709, 1993
A;Title: Diversity within natural populations of eastern equine encephalomyelitis virus.
A;Reference number: A48608; MUID: 93331728; PMID: 8101674
A;Accession: B48608
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-207 <WFA>
A;Cross-references: GB:S63996; NID:9400551; PIDN:AAB27576.1; PID:9400552
A;Note: Sequence extracted from NCBI backbone (NCBIN:135481; NCBIP:135482)
C;Superfamily: togavirus structural polyprotein
C;Keywords: glycoprotein

Query Match Score 32; DB 2; Length 207;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 143 CRGDC 147

RESULT 7

D85098

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OM protein - protein search, using sw model

Run on: September 22, 2004, 06:46:27 ; Search time 39 Seconds

(without alignments) 12.332 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

PIR 78:
1: pir1:
2: pir2:
3: pir3:
4: pir4:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	35	100.0	350	2	T25451		transforming growth factor beta homolog - Caenorhabditis elegans
2	35	100.0	373	2	PW0042		activin - fruit fly (Drosophila sp.) (fragment)
3	35	100.0	1076	2	T26044		protein C34G6.6 [i]
4	32	91.4	75	2	B42206		structural polypopro
5	32	91.4	132	2	T43370		structural polypopro
6	32	91.4	207	2	A48608		hypothetical prote
7	32	91.4	210	2	D83098		E1 glyccoprotein -
8	32	91.4	441	2	S42284		hypothetical prote
9	32	91.4	654	2	S53805		growth/differentia
10	32	91.4	690	2	T11749		beta glucosidase/x
11	32	91.4	1011	2	C87789		transferrin - Atla
12	32	91.4	1239	1	VHVVVE		protein
13	32	91.4	1240	1	VHVVVE		protein C34G6.6 [i]
14	32	91.4	1241	2	S26373		structural polypro
15	32	91.4	1242	2	S72350		genomic polypepti
16	32	91.4	1242	1	A56605		structural polypro
17	32	91.4	1254	1	VHWVVE		structural polypro
18	32	91.4	1254	1	VHWVVT		structural polypro
19	32	91.4	1254	1	JQ1978		structural polypro
20	32	91.4	1254	1	JQ1979		structural polypro
21	32	91.4	1255	1	B44213		structural polypro
22	32	91.4	1255	1	D44213		structural polypro
23	32	91.4	2090	2	T30075		hypothetical prote
24	32	91.4	2153	2	T30074		hypothetical prote
25	31	88.6	80	2	F833128		hypothetical prote
26	31	88.6	154	2	A96544		hypothetical prote
27	31	88.6	247	2	F71545		probable oligopept
28	31	88.6	249	1	S47153		type IV preillin p
29	31	88.6	342	2	H86300		F19K19.12 protein p

SUMMARY

A;Gene: daf-7

A;Map Position: 3

A;Introns: 43/3; 123/3; 184/2; 288/3

C;Superfamily: inhibin

RESULT 1

T25451

transforming growth factor beta homolog - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_change 15-Oct-1999 #text_change 17-Mar-2000

C;Accession: T25451

R:Bentley, D.

Submitted to the EMBL Data Library, December 1996

A;Description: The sequence of C. elegans cosmid B0412.

A;Reference number: Z22037

A;Accession: T25451

A;Status: Preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-350 <BEN>

A;Cross-references: EMBL:U80953; PIDN:AAB52554.1; GSPDB:GN00021

A;Experimental source: strain Bristol N2; Clone B0412

C;Genetics:

A;Gene: daf-7

A;Map Position: 3

A;Introns: 43/3; 123/3; 184/2; 288/3

C;Superfamily: inhibin

RESULT 2

T25451

activin - fruit fly (Drosophila sp.) (fragment)

C;Species: Drosophila sp.

C;Date: 18-Jun-1998 #sequence_change 10-Jul-1998 #text_change 17-Nov-2000

C;Accession: PW0042

R;Kutty, G.; Kutty, R. K.; Samuel, W.; Duncan, T.; Jaworski, C.; Wiggert, B.

Biochem Biophys Res Commun. 246, 644-649, 1998

A;Title: Identification of a new member of transforming growth factor-beta superfamily in

A;Reference number: PW0042; MUID:98289585; PMID:9618266

A;Accession: PW0042

A;Molecule type: tRNA

A;Residues: 1-373 <KNT>

A;Cross-references: GB:AF054822

C;Genetics:

A;Cross-references: FlyBase:FBgn0024913

A;Start codon: GCT

A;Introns: 86/3

C;Superfamily: inhibin

Query Match 100.0%; Score 35; DB 2; Length 350;

Query Match 100.0%; Score 35; DB 2; Length 350;

Query Match 100.0%; Score 35; DB 2; Length 350;

Query Match 100.0%; Score 35; DB 2; Length 350;

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US-08-335-832-41
Query Match Similarity 74.3%; Score 26; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Other Information: ACETYLATION

Qy      2 RGDC 5
Db      1 RGDC 4

RESULT 14
US-08-753-781-34
Sequence 34, Application US/08753781C
Patent No. 5951981
GENERAL INFORMATION:
APPLICANT: Markland Jr., Francis S.
APPLICANT: Bush, Larry R.
APPLICANT: Swenson, Stephen
APPLICANT: Flores Sanchez, Bladío
TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
FILE REFERENCE: DITI 124
CURRENT APPLICATION NUMBER: US/08/753,781C
CURRENT FILING DATE: 1996-12-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 4

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: ACETYLATION

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: AMIDATION

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:synthetic
US-08-753-781-34

Query Match Similarity 74.3%; Score 26; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0; Other Information: ACETYLATION
Job time : 18 secs

Qy      2 RGDC 5
Db      1 RGDC 4

RESULT 15
US-09-141-127-14
Sequence 14, Application US/09141127A
Patent No. 6083481
GENERAL INFORMATION:
APPLICANT: Lister-James, John
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: THROMBUS IMAGING AGENTS
FILE REFERENCE: DITI 113-1USCI
CURRENT APPLICATION NUMBER: US/09/141,127A
CURRENT FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 08/335,832
EARLIER FILING DATE: 1995-01-05
EARLIER APPLICATION NUMBER: PCT/US93/04794
EARLIER FILING DATE: 1993-05-21
EARLIER APPLICATION NUMBER: 07/886,752
EARLIER FILING DATE: 1992-05-21
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 14
LENGTH: 4

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; MOLECULE TYPE: peptide
; FEATURE: Modified-site
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Cys is Ac-Cys."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Modified-site
; OTHER INFORMATION: /note= "Asp is Asp-penicillamine"
; US-08-240-711-4

Query Match      74.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CRGD 4
     |||
Db    1 CRGD 4

RESULT 12
US-08-457-753-4
; Sequence 4; Application US/08457753
; Patent No. 5759512
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTHONY J.
; TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESS: Brody and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,753
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/240,711
; FILING DATE: 12-JUL-1994
; APPLICATION NUMBER: PCT/US92/09713
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,177
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,179
; FILING DATE: 08-NOV-1991
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-658-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

; FEATURE: Modified-site
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Acetyl
; OTHER INFORMATION: /note= "The amino terminus is modified by covalent
; linkage to an acetyl group."
; US-08-457-753-4

Query Match      74.3%; Score 26; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 CRGD 4
     |||
Db    1 CRGD 4

RESULT 13
US-08-335-832-41
; Sequence 41; Application US/08335832
; Patent No. 5953311
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Libter-James, John
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; Thrombus Imaging
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive Suite 3000
; CITY: Chicago
; STATE: Illinois
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,832
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5925331man, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,216-I
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Amide
; OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
; amide."
; US-08-335-832-41

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,002
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/625,695
; FILING DATE: 03-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,186
; FILING DATE: 11-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2748
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: both
US-08-924-002-10

RESULT 9
Query Match Score 100.0%; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Delins 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

; ISRAEL F.
; TITLE OF INVENTION: PLATELET AGGREGATION INHIBITORS
; NUMBER OF SEQUENCES: 93
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/483,229
; FILING DATE: 20-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 418,028
; FILING DATE: 06-OCT-1989
; APPLICATION NUMBER: 367,509
; FILING DATE: 16-JUN-1989
; SEQ ID NO:77:
; LENGTH: 5
5318899-77

RESULT 9
Query Match Score 91.4%; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Delins 0;

Qy 1 CRGDC 5
Db 1 CKGDC 5

; Liu, Shuang
; TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
; FILE REFERENCE: BMS-2207
; CURRENT APPLICATION NUMBER: US/09/660,377A
; CURRENT FILING DATE: 2000-09-12

RESULT 10
US-09-660-377A-11
; Sequence 11, Application US/09660377A
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: Macrocyclic Chelants For Metallopharmaceuticals
; FILE REFERENCE: BMS-2207
; CURRENT APPLICATION NUMBER: US/09/660,377A
; CURRENT FILING DATE: 2000-09-12

; PRIOR APPLICATION NUMBER: 60/153,512
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO: 11
; SOFTWARE: PatentIn version 3.2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(5)
; OTHER INFORMATION: Cyclo
US-09-660-377A-11

RESULT 11
Query Match Score 85.7%; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Delins 1;

Qy 1 CRGDC 5
Db 1 CNGDC 5

; PRIOR APPLICATION NUMBER: US/08-240-711-4
; PRIOR FILING DATE: 06-NOV-1992
; NUMBER OF SEQ ID NOS: 22
; SEQ ID NO: 5679777
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; ZIP: 20004
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,711
; FILING DATE: 12-JUL-1994
; CLASIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PC/US92/09713
; FILING DATE: 06-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,177
; FILING DATE: 08-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,179
; FILING DATE: 08-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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QY      1 CRGDC 5 ; TELEFAX: (619) 535-8949
Db      1 CRGDC 5 ; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-753-781-35 ; SEQ ID NO: 35

RESULT 5
; Sequence 35, Application US/08753781C
; Patent No. 5951981
; GENERAL INFORMATION:
; APPLICANT: Markland Jr., Francis S.
; APPLICANT: Bush, Larry R.
; APPLICANT: Swenson, Stephen
; APPLICANT: Flores Sanchez, Bladimir
; TITLE OF INVENTION: THROMBOLYTIC AGENTS WITH ANTITHROMBOTIC ACTIVITY
; FILE REFERENCE: DTTI 124
; CURRENT APPLICATION NUMBER: US/08/753,781C
; CURRENT FILING DATE: 1996-12-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: Peptide
US-08-753-781-35

Query Match
Best Local Similarity 100.0%; Score 35; DB 2; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORGANISM: Artificial Sequence
; TYPE: PRT
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBOLYTIC AGENTS
; FILE REFERENCE: DTTI 113-1USCI
; CURRENT APPLICATION NUMBER: US/09/141,127A
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: Peptide
US-09-141-127-15

RESULT 6
; Sequence 37, Application US/08286861
; Patent No. 5984478
; GENERAL INFORMATION:
; APPLICANT: Koivunen, Erkki
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: No. 5981478el Integrin-Binding Peptides
; NUMBER OF SEQUENCES: 46
; CURRENT APPLICATION NUMBER: US/08/286,861
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release' #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

RESULT 7
; Sequence 15, Application US/09141127A
; Patent No. 6081481
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; APPLICANT: Dean, Richard T.
; APPLICANT: Lister-James, John
; TITLE OF INVENTION: THROMBOLYTIC AGENTS
; FILE REFERENCE: DTTI 113-1USCI
; CURRENT APPLICATION NUMBER: US/09/141,127A
; CURRENT FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 08/335,832
; EARLIER FILING DATE: 1995-01-05
; EARLIER APPLICATION NUMBER: PCT/US93/04794
; EARLIER FILING DATE: 1993-05-21
; EARLIER APPLICATION NUMBER: 07/886,752
; EARLIER FILING DATE: 1992-05-21
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: Peptide
US-09-141-127-15

RESULT 8
; Sequence 10, Application US/089244002
; Patent No. 6177542
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki I.
; APPLICANT: Koivunen, Erkki
; TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION NUMBER: US/08/286,861
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release' #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,861
FILING DATE: 04-AUG-1994
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/158,001
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```

Sequence 8, Application US/08425238
 / Patent No. 5627263
 / GENERAL INFORMATION:
 / APPLICANT: Ruoslahti, Erkki
 / ATTORNEY/AGENT INFORMATION:
 / TITLE OF INVENTION: No. 5627263el Integrin-Binding Peptides
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Campbell and Flores
 / STREET: 4370 La Jolla Village Drive, Suite 700
 / CITY: San Diego
 / STATE: California
 / COUNTRY: USA
 / ZIP: 92112
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/425,238
 / FILING DATE:
 / CLASSIFICATION: 514
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/158,001
 / FILING DATE: 24-NOV-1993
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Campbell, Cathryn A.
 / REGISTRATION NUMBER: 31,815
 / REFERENCE/DOCKET NUMBER: P-LA 9775
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (619) 535-9001
 / TELEFAX: (619) 535-8949
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-425-238-8

Query Match Score 35; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 3
 US-08-625-695A-10
 / Sequence 10, Application US/08625695A
 / Patent No. 5912234
 / GENERAL INFORMATION:
 / APPLICANT: Ruoslahti, Erkki I.
 / ATTORNEY/AGENT INFORMATION:
 / TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 / NUMBER OF SEQUENCES: 27
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: CAMPBELL & FLORES, LLP
 / STREET: 4370 La Jolla Village Drive, Suite 700
 / CITY: San Diego
 / STATE: California
 / COUNTRY: United States
 / ZIP: 92112
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/625,695A

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 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

FILING DATE: 03-APR-1996
 / CLASSIFICATION: 530
 / PRIORITY APPLICATION DATA:
 / APPLICATION NUMBER: US 08/212,146
 / FILING DATE: 11-MAR-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Campbell, Cathryn A.
 / REGISTRATION NUMBER: 31,815
 / REFERENCE/DOCKET NUMBER: P-LA 2041
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (619) 535-0001
 / TELEFAX: (619) 535-8949
 / INFORMATION FOR SEQ ID NO: 10:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5 amino acids
 / TYPE: amino acid
 / TOPOLOGY: both
 / US-08-625-695A-10

Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 4
 US-08-335-832-42
 / Sequence 42, Application US/083335832
 / Patent No. 5925331
 / GENERAL INFORMATION:
 / APPLICANT: Dean, Richard T.
 / ATTORNEY/AGENT INFORMATION:
 / TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 / NUMBER OF SEQUENCES: 53
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Banner & Allegretti, Ltd.
 / STREET: 10 South Wacker Drive Suite 3000
 / CITY: Chicago
 / STATE: Illinois
 / COUNTRY: USA
 / ZIP: 60606
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/335,832
 / FILING DATE: 05-JAN-1995
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: No. 5925331iran, Kevin E
 / REGISTRATION NUMBER: 35,303
 / REFERENCE/DOCKET NUMBER: 94,216-1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 312-715-1000
 / TELEFAX: 312-715-1234
 / INFORMATION FOR SEQ ID NO: 42:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / US-08-335-832-42

Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 3e+05;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

GenCore version 5.1.6
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on: September 22, 2004, 07:06:24 ; Search time 17 Seconds
 (without alignments)
 15.184 Million Cell. updates/sec

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select score: 35

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ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 389414 seqs, 51625971 residues

1 number of hits satisfying chosen parameters: 24558

num DB seq length: 0

num DB seq length: 5

-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

base : Issued_Patents_AA:^{*}

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 2: /cgm2_6/prodata/2/iaa/5B_COMB_pep:
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 4: /cgm2_6/prodata/2/iaa/6B_COMB_pep:
 5: /cgm2_6/prodata/2/iaa/PCTUS_COMB_pep:
 6: /cgm2_6/prodata/2/iaa/backfiles1.pep:^{*}

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

RESULT 1
 US-08-212-186A-10
 Sequence 10, Application US/08212186A
 Patent No. 5536814
 GENERAL INFORMATION:
 APPLICANT: Ruoislantti, Eirki I.
 APPLICANT: Koivunen, Eirki
 TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/212,186A
 FILING DATE: 11-MAR-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Kathryn A.
 REGISTRATION NUMBER: 31,815
 REFERENCE/DOCKET NUMBER: P-LA 9861
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 10:
 SEQENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 US-08-212-186A-10

Query Match Length DB ID Description

Query	Match	Length	DB	ID	Description
1	35	100.0	5	1	US-08-212-186A-10 Sequence 10, Appl
2	35	100.0	5	1	US-08-425-1238-8 Sequence 8, Appl
3	35	100.0	5	2	US-08-625-695A-10 Sequence 42, Appl
4	35	100.0	5	2	US-08-335-832-42 Sequence 35, Appl
5	35	100.0	5	2	US-08-781-35 Sequence 37, Appl
6	35	100.0	5	2	US-08-286-861-37 Sequence 15, Appl
7	35	100.0	5	3	US-09-141-127-15 Sequence 10, Appl
8	35	91.4	5	3	US-08-924-002-10 Patient No. 5318899 Sequence 11, Appl
9	30	85.7	5	4	US-09-660-377A-11 Sequence 4, Appl
10	26	74.3	4	1	US-08-240-711-4 Sequence 4, Appl
11	26	74.3	4	1	US-08-475-753-4 Sequence 4, Appl
12	26	74.3	4	2	US-08-335-832-41 Sequence 41, Appl
13	26	74.3	4	2	US-08-753-781-34 Sequence 14, Appl
14	26	74.3	4	3	US-09-141-127-14 Sequence 1, Appl
15	26	74.3	4	3	US-08-960-054A-1 Sequence 1, Appl
16	26	74.3	4	3	US-08-4787-1 Sequence 1, Appl
17	26	74.3	5	1	US-08-475-751-1 Sequence 1, Appl
18	26	74.3	5	1	US-08-406-862-1 Sequence 1, Appl
19	26	74.3	4	4	US-08-925-715-4 Patient No. 5384309 Sequence 1, Appl
20	26	74.3	4	6	US-08-882-880-1 Sequence 1, Appl
21	26	74.3	5	1	US-07-885-202A-1 Sequence 1, Appl
22	26	74.3	5	1	US-08-425-787-1 Sequence 1, Appl
23	26	74.3	5	1	US-08-475-751-1 Sequence 1, Appl
24	26	74.3	5	1	US-08-406-862-1 Sequence 1, Appl
25	26	74.3	5	1	US-08-493-935-1 Sequence 1, Appl
26	26	74.3	5	1	US-08-482-880-1 Sequence 1, Appl
27	26	74.3	5	2	US-08-273-274-1 Sequence 3, Appl

SUMMARIES

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6	35	100.0	5	2
7	35	100.0	5	3
8	35	100.0	5	3
9	32	91.4	5	6
10	30	85.7	5	4
11	26	74.3	4	1
12	26	74.3	4	1
13	26	74.3	4	2
14	26	74.3	4	2
15	26	74.3	4	3
16	26	74.3	4	3
17	26	74.3	4	3
18	26	74.3	5	1
19	26	74.3	5	1
20	26	74.3	4	4
21	26	74.3	4	4
22	26	74.3	4	4
23	26	74.3	5	1
24	26	74.3	5	1
25	26	74.3	5	1
26	26	74.3	4	4
27	26	74.3	4	4
28	26	74.3	5	2

Query Match Best Local Similarity Score 35; DB 1; Length 5;
 Matches 5; Conservative 0; Mismatches 0; Index 18 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 2
 US-08-482-880-1

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RESULT 14
US-10-853-895-3
; Sequence 3, Application US/10853895

; GENERAL INFORMATION:
; APPLICANT: Ponzoni, Marco
; APPLICANT: Corti, Angelo
; APPLICANT: Allen, Theresa
; TITLE OF INVENTION: TUMOR TARGETED DRUG DELIVERY SYSTEMS AND USES THEREOF
FILE REFERENCE: 11464-006-999 (108463-999004)
CURRENT APPLICATION NUMBER: US/10/853,895
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: GB 0312309.8
PRIOR FILING DATE: 2003-05-29
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 3 LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
US-10-853-895-3

Query Match Similarity 62.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
Qy 1 CRGDC 5
Db 1 CNGRC 5

RESULT 15
US-10-287-811A-12
; Sequence 12, Application US/10287811A
; GENERAL INFORMATION:
; APPLICANT: Molimed Spa
; FILE REFERENCE: P014717USM CLM
; CURRENT APPLICATION NUMBER: US/10/287,811A
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: IT MI2000A000249
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: C.I.P from US 10/218,906
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
SEQ ID NO 12 LENGTH: 5
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: ligand

FEATURE:
NAME/KEY: UNSURE
LOCATION: (1) ..(5)
OTHER INFORMATION: where peptide is cyclic or linear
US-10-287-811A-12

Query Match Similarity 62.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0;
Gaps 0;
Qy 1 CRGDC 5
Db 1 CNGRC 5

Search completed: September 22, 2004, 07:19:49
Job time : 64 secs

US-10-714-564A-259
; Sequence 259, Application US/10714564A
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Michaud, Stephanie D.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; FUNCTIONS OF NONCLASSICAL CADHERINS
; FILE REFERENCE: 100096_418
; CURRENT APPLICATION NUMBER: US/10/714_564A
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 1402
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Exemplary cyclic peptide
; US-10-714-564A-259

Query Match 71.4%; Score 25; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGWC 5

RESULT 11
US-10-785-924-3
; Sequence 3, Application US/10785924
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; ALZHEIMER'S DISEASE
; FILE REFERENCE: 0054-1092-012
; CURRENT APPLICATION NUMBER: US/10/785_924
; CURRENT FILING DATE: 2004-02-24
; PRIOR APPLICATION NUMBER: US 09/866,898
; PRIOR FILING DATE: 2001-05-29
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: US 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
; US-10-785-924-3

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Best Local Similarity 60.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGAC 5

RESULT 12
PCT-US04-29095-2
; Sequence 2, Application PC/TUS0429095
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of Colorado
; APPLICANT: Koch, Ted

Query Match 62.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CNGRC 5

RESULT 13
US-10-839-037-37
; Sequence 37, Application US/10839037
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID HORMONE
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/10/839_037
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: US/09/843,221A
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/265,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR APPLICATION NUMBER: 60/214,860
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified bovine PTH
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 37

Query Match 62.9%; Score 22; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 6.5e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

<p>Db 1 RGDC 4</p> <p>Qy 2 RGDC 5</p> <p>Db 2 RGDC 5</p> <p>Qy 2 RGDC 5</p>	<p>RESULT 6</p> <p>US-10-111-983-4826 ; Sequence 4826, Application US/10111983 ; GENERAL INFORMATION: ; APPLICANT: CHIRON SpA ; APPLICANT: GALEOTTI Cesira ; APPLICANT: GRANDI Guido ; APPLICANT: MASTIGNANI Vega ; APPLICANT: MORA Mariarosa ; APPLICANT: PIZZA Mariagrazia ; APPLICANT: RAPPOLI Rino ; APPLICANT: RATTI Giulio ; APPLICANT: SCARLETTI Maria ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES ; FILE REFERENCE: 2300-1654 (PP01654_003) ; CURRENT APPLICATION NUMBER: US/10/111,983 ; CURRENT FILING DATE: 2003-06-27 ; PRIOR FILING DATE: 1999-10-29 ; NUMBER OF SEQ ID NOS: 37764 ; SOFTWARE: SeqWin99, version 1.02 ; SEQ ID NO: 4826 ; LENGTH: 5 ; TYPE: PRT ; ORGANISM: Neisseria ; US-10-111-983-4826</p> <p>Query Match 74.3%; Score 26; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 6.5e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 2 RGDC 5 Db 2 RGDC 5</p> <p>RESULT 7</p> <p>US-10-111-983-18704 ; Sequence 18704, Application US/10111983 ; GENERAL INFORMATION: ; APPLICANT: CHIRON SpA ; APPLICANT: GALEOTTI Cesira ; APPLICANT: GRANDI Guido ; APPLICANT: MASTIGNANI Vega ; APPLICANT: PIZZA Mariagrazia ; APPLICANT: RAPPOLI Rino ; APPLICANT: RATTI Giulio ; APPLICANT: SCARLETTI Maria ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES ; FILE REFERENCE: 2300-1654 (PP01654_003) ; CURRENT APPLICATION NUMBER: US/10/111,983 ; CURRENT FILING DATE: 2003-06-27 ; PRIOR FILING DATE: 1999-10-29 ; NUMBER OF SEQ ID NOS: 37764 ; SOFTWARE: SeqWin99, version 1.02 ; SEQ ID NO: 18704 ; LENGTH: 5 ; TYPE: PRT ; ORGANISM: Neisseria ; US-10-111-983-18704</p> <p>Query Match 74.3%; Score 26; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 6.5e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>
<p>Db 2 RGDC 5</p> <p>Qy 2 RGDC 5</p>	<p>RESULT 8</p> <p>US-10-111-983-30763 ; Sequence 30763, Application US/10111983 ; GENERAL INFORMATION: ; APPLICANT: CHIRON SpA ; APPLICANT: GALEOTTI Cesira ; APPLICANT: GRANDI Guido ; APPLICANT: MASTIGNANI Vega ; APPLICANT: MORA Mariarosa ; APPLICANT: PIZZA Mariagrazia ; APPLICANT: RAPPOLI Rino ; APPLICANT: RATTI Giulio ; APPLICANT: SCARLETTI Maria ; TITLE OF INVENTION: NEISSERIAL ANTIGENIC PEPTIDES ; FILE REFERENCE: 1300-1654 (PP01654_003) ; CURRENT APPLICATION NUMBER: US/10/111,983 ; CURRENT FILING DATE: 2003-06-27 ; PRIOR APPLICATION NUMBER: US-60/162616 ; PRIOR FILING DATE: 1999-10-29 ; NUMBER OF SEQ ID NOS: 37764 ; SOFTWARE: SeqWin99, version 1.02 ; SEQ ID NO: 30763 ; LENGTH: 5 ; TYPE: PRT ; ORGANISM: Neisseria ; US-10-111-983-30763</p> <p>Query Match 74.3%; Score 26; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 6.5e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>RESULT 9</p> <p>US-10-869-355-8 ; Sequence 8, Application US/10869355 ; GENERAL INFORMATION: ; APPLICANT: Zhang, Dongxiao ; TITLE OF INVENTION: METHODS OF SCREENING FOR MONOCLONAL ; ANTIBODIES WITH DESIRABLE ACTIVITY ; FILE REFERENCE: EPIT-007 ; CURRENT APPLICATION NUMBER: US/10/869,355 ; CURRENT FILING DATE: 2004-06-15 ; PRIOR APPLICATION NUMBER: 60/483,391 ; PRIOR FILING DATE: 2003-06-26 ; PRIOR APPLICATION NUMBER: 60/484,185 ; PRIOR FILING DATE: 2003-06-30 ; NUMBER OF SEQ ID NOS: 38 ; SOFTWARE: FastSeq For Windows Version 4.0 ; SEQ ID NO: 8 ; LENGTH: 5 ; TYPE: PRT ; ORGANISM: Oryctolagus cuniculus ; US-10-869-355-8</p> <p>Query Match 74.3%; Score 26; DB 6; Length 5; Best Local Similarity 100.0%; Pred. No. 6.5e+05; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>
<p>Db 2 RGDC 5</p> <p>Qy 2 RGDC 5</p>	<p>RESULT 10</p>

```

TITLE OF INVENTION: METHODS
FILE REFERENCE: TSRI-987.1PC
CURRENT APPLICATION NUMBER: PCT/US04/132212
PRIORITY FILING DATE: 2004-05-05
PRIOR APPLICATION NUMBER: 60/467,188
PRIOR FILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
Cys1 and Cys5
PCT-US04-1322-13
Query Match 82.9%; Score 29; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRADC 5

RESULT 3
US-10-836-289-13
Sequence 13, Application US/10836289
GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: FRIEDLANDER, Martin
APPLICANT: DORRELL, Michael I.
TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND
FILE REFERENCE: TSRI-987.1
CURRENT APPLICATION NUMBER: US/10/836,289
PRIORITY FILING DATE: 2004-04-30
PRIOR APPLICATION NUMBER: 60/467,188
PRIOR FILING DATE: 2003-05-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CYCLIC CADHERIN ANTAGONIST, DISULFIDE BOND BETWEEN
Cys1 and Cys5
US-10-836-289-13
Query Match 82.9%; Score 29; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRADC 5

RESULT 4
US-10-475-104-1
Sequence 1, Application US/10475104
GENERAL INFORMATION:
APPLICANT: Schneider-Mergener, Jens
APPLICANT: Schutkowski, Mike
APPLICANT: Reimer, Ulf
APPLICANT: Dong, Liying
APPLICANT: Panske, Storen
APPLICANT: Scharn, Dirk
APPLICANT: Osterkamp, Frank
APPLICANT: Hummel, Gerd
APPLICANT: Jobron, Laurence
APPLICANT: 
TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
FILE REFERENCE: 2918-0102
CURRENT APPLICATION NUMBER: US/10/475,104
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/EP02/04265
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: cell-adhesive peptide
US-10-475-104-1
Query Match 74.3%; Score 26; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RGDC 5
Db 1 RGDC 4

RESULT 5
US-10-734-730-4
Sequence 4, Application US/10734730
GENERAL INFORMATION:
APPLICANT: Klaveren, Jo
APPLICANT: Rongved, Pal
APPLICANT: Hogset, Anders
APPLICANT: Tolleshaug, Helge
APPLICANT: Cuthbertson, Alan
APPLICANT: Godal, Aslak
APPLICANT: Hoff, Lars
APPLICANT: Gogstad, Geir
APPLICANT: Bryn, Klaus
APPLICANT: Naevestad, Anne
APPLICANT: Lovhaug, Dagfinn
APPLICANT: Hillebust, Halldis
APPLICANT: Solbakken, Magne
TITLE OF INVENTION: Diagnostic/therapeutic Agents
FILE REFERENCE: NIDN-10314
CURRENT APPLICATION NUMBER: US/10/734,730
CURRENT FILING DATE: 2003-12-15
PRIOR APPLICATION NUMBER: 09/925,715
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 08/959,206
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/049,263
PRIOR FILING DATE: 1997-06-07
PRIOR APPLICATION NUMBER: 60/049,264
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/049,266
PRIOR FILING DATE: 1997-06-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 4
TYPE: PRT
ORGANISM: Synthetic RGDC sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic RGDC sequence
US-10-734-730-4
Query Match 74.3%; Score 26; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RGDC 5
Db 1 RGDC 4

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Inc.

OM protein - protein search, using sw model

Run on: September 22, 2004, 07:08:54 ; Search time 62 Seconds

(without alignments)
10.974 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 735861 seqs, 136079791 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Pending Patents_AA_New.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	30	85.7	5 6	US-10-342-081-77
2	29	82.9	5 6	PCT-US04-13212-13
3	29	82.9	5 6	US-10-036-289-13
4	26	74.3	4 6	US-10-475-004-1
5	26	74.3	4 6	US-10-734-270-4
6	26	74.3	5 6	US-10-111-983-4826
7	26	74.3	5 6	US-10-111-983-18704
8	26	74.3	5 6	US-10-111-983-30763
9	26	74.3	5 6	US-10-169-355-8
10	25	71.4	5 6	US-10-714-564A-259
11	24	68.6	5 6	US-10-785-924-3
12	22	62.9	5 1	PCT-US04-20905-2
13	22	62.9	5 6	US-10-839-037-37
14	22	62.9	5 6	US-10-853-095-3
15	22	62.9	5 6	US-10-878-811A-12
16	22	62.9	5 6	US-10-900-199-24
17	22	62.9	5 6	US-10-912-064-37
18	22	62.9	5 6	US-10-712-298-24
19	22	62.9	5 6	US-10-027-649-223
20	21	60.0	4 6	US-10-815-614-41
21	21	60.0	4 6	US-10-877-930-41
22	21	60.0	5 6	US-10-111-983-7553
23	21	60.0	5 6	US-10-111-983-20982
24	21	60.0	5 6	US-10-111-983-33204
25	21	60.0	5 6	US-10-712-025-384
26	20	57.1	5 6	US-10-665-468A-3

Result 1

US-10-342-081-77

; Sequence 77, Application US-10342081

; GENERAL INFORMATION:

; APPLICANT: Rijopadhye, Milind

; APPLICANT: Edwards, D. Scott

; APPLICANT: Barrett, John A.

; APPLICANT: Carpenter, Jr., Alan P.

; APPLICANT: Harris, Thomas D.

; APPLICANT: Hemingway, Stuart J.

; APPLICANT: Liu, Shuang

; APPLICANT: Singh, Prahlad R.

; TITLE OF INVENTION: PHARMACEUTICALS FOR THE IMAGING OF ANGIOGENIC DISORDERS

; FILE REFERENCE: BMS-2024

; CURRENT APPLICATION NUMBER: US-10/342,081

; CURRENT FILING DATE: 2003-01-14

; PRIOR APPLICATION NUMBER: US 09/599,295

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOs: 169

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 77

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: MISC_FEATURE

; LOCATION: (1)-(5)

; OTHER INFORMATION: cyclic amino acid

; SEQ ID NO: 77

RESULT 2

PCT-US04-13212-13

; Sequence 13, Application PC/TUS0413212

; GENERAL INFORMATION:

; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE

; APPLICANT: FRIEDLANDER, Martin

; APPLICANT: DORRELL, Michael I.

; TITLE OF INVENTION: SELECTIVE R-CADHERIN ANTAGONISTS AND

ALIGNMENTS

```

; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Synthetic Construct
us-10-033-769-11

Query Match 85.7%; Score 30; DB 26; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 CRGDC 5
          | |||
Db      1 CNGDC 5

```

```

RESULT 15
us-10-081-258-11
; Sequence 11, Application US/10081258
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: Ascorbic Acid Analogs For Metalloradiopharmaceuticals
; FILE REFERENCE: PH-7277 US (BMS-0746)
; CURRENT APPLICATION NUMBER: US/10/081.258
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/271,389
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 5
; TYPE: PRT
; FEATURE: Artificial Sequence
; OTHER INFORMATION: Synthetic construct
us-10-081-258-11

Query Match 85.7%; Score 30; DB 26; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      1 CRGDC 5
          | |||
Db      1 CNGDC 5

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Search completed: September 22, 2004, 07:18:39
Job time : 403 secs

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; Sequence 9, Application US/09912609
; GENERAL INFORMATION:
; APPLICANT: UNGER, EVAN C.
; APPLICANT: MATSUNAGA, TERRY ONICHI
; APPLICANT: RAMASWAMI, VARADARAJAN
; APPLICANT: ROMANOWSKI, MAREK J.
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 5030-0001.24
; CURRENT APPLICATION NUMBER: US/09/912,609
; CURRENT FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 09/703,474
; PRIORITY FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 09/478,124
; PRIORITY FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-912-609-9

Query Match          100.0%; Score 35; DB 24; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 CRGDC 5
Qy          1 CRGDC 5
Db          1 CRGDC 5

RESULT 11
US-10-304-160-2
; Sequence 2, Application US/10304160
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J
; APPLICANT: KOVESDI, IMRE
; APPLICANT: ROELVINK, PETRUS W
; APPLICANT: BINFIELD, DAVID
; APPLICANT: BROUH, DOUGLAS E
; APPLICANT: LIZONNOVA, ALENA
; TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
; FILE REFERENCE: 220148
; CURRENT APPLICATION NUMBER: US/10/304,160
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: PCT/US01/17391
; PRIORITY FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: US 09/631,191
; PRIORITY FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/208451
; PRIORITY FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-304-160-2

Query Match          100.0%; Score 35; DB 29; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 CRGDC 5
Qy          1 CRGDC 5
Db          1 CRGDC 5

RESULT 12
US-60-208-451-2
; Sequence 2, Application US/60208451
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, Thomas J
; APPLICANT: Kovessdi, Imre
; APPLICANT: Roelvink, Petrus W
; APPLICANT: Binfield, David
; APPLICANT: Brough, Douglas E
; APPLICANT: Lizonova, Alena
; TITLE OF INVENTION: ALTERNATIVELY TARGETED ADENOVIRUS
; FILE REFERENCE: 205046
; CURRENT APPLICATION NUMBER: US/60/208,451
; CURRENT FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-208-451-2

Query Match          100.0%; Score 35; DB 33; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          1 CRGDC 5
Qy          1 CRGDC 5
Db          1 CRGDC 5

RESULT 13
US-09-995-388-48
; Sequence 48, Application US/09995388
; GENERAL INFORMATION:
; APPLICANT: Carpenter, Jr., Alan P.
; TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
; FILE REFERENCE: BMS-2201
; CURRENT APPLICATION NUMBER: US/09/995,388
; CURRENT FILING DATE: 2001-11-17
; PRIOR APPLICATION NUMBER: US 60/253,324
; PRIORITY FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-995-388-48

Query Match          85.7%; Score 30; DB 25; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.5e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db          1 CNGDC 5
Qy          1 CNGDC 5
Db          1 CNGDC 5

RESULT 14
US-10-033-769-11
; Sequence 11, Application US/10033769
; GENERAL INFORMATION:
; APPLICANT: Liu, Shuang
; TITLE OF INVENTION: POLYPODAL CHELANTS FOR METALLOPHARMACEUTICALS
; FILE REFERENCE: BMS-2204
; CURRENT APPLICATION NUMBER: US/10/033,769
; CURRENT FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: US 60/260,619
; PRIORITY FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
US-10-033-769-11

```

RESULT 7
US-09-364-597A-37
Sequence 37, Application US/09364597A
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Novel Integrin-Binding Peptides
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/364,597A
FILING DATE: 30-JUL-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,001
FILING DATE: 24-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,861
FILING DATE: 04-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 3419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (858) 535-9001
TELEFAX: (858) 535-8949
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: circular

US-09-364-597A-37
Query Match 100.0%; Score 35; DB 17; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 8
US-09-627-035-10
Sequence 10, Application US/09627035
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

US-09-627-035-10
Query Match 100.0%; Score 35; DB 20; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+06; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CRGDC 5

RESULT 10
US-09-912-609-9

TITLE OF INVENTION: NOVEL INTEGRIN-BINDING PEPTIDES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/625,695
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.
 REGISTRATION NUMBER: 31,815
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEX/FAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: both
 US-08-625-695-10

Query Match Score 100.0%; Pred. No. 5.5e+06; Length 5;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 5
 US-08-753-781B-45
 / Sequence 45, Application US/08753781B
 / GENERAL INFORMATION:
 / APPLICANT: Markland Jr., Francis S.
 / APPLICANT: Bush, Larry R.
 / APPLICANT: Swenson, Stephen
 / APPLICANT: Flores Sanchez, Eladio
 / TITLE OF INVENTION: THROMBOLYtic AGENTS WITH ANTITHROMBOTIC
 / NUMBER OF SEQUENCES: 54
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Diatide, Inc.
 / STREET: 9 Delta Drive
 / CITY: Londonderry
 / STATE: NH
 / COUNTRY: USA
 / ZIP: 03053
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/982,981
 / FILING DATE:
 / PRIORITY/SEQUENCE INFORMATION:
 / NAME: McDaniel, Patricia A.
 / REGISTRATION NUMBER: 33,194
 / REFERENCE/DOCKET NUMBER: DITI 124.1
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 603 437 8970
 / TELEX/FAX: 603 437 8970
 / INFORMATION FOR SEQ ID NO: 45:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 5 amino acids
 / TYPE: amino acid
 / STRANDEDNESS:
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / US-08-982-981-45

Query Match Score 100.0%; Pred. No. 5.5e+06; Length 5;
 Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/158, 001
 FILING DATE: 24-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: HOOK, Gregory
 REGISTRATION NUMBER: 38,701
 REFERENCE DOCKET NUMBER: FP-LA 1220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEX/FAX: (619) 535-8949

SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: circular

PCT-US94-13542-37

RESULT 2
 US-07-961-889-55
 Sequence 55, Application US/07961889
 GENERAL INFORMATION:
 APPLICANT: Lobi, Thomas J.
 ADDRESSSEE: Chiang, Shiu-Jan
 APPLICANT: Cardarelli, Pina M.
 TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 NUMBER OF SEQUENCES: 223

Query Match 100.0%; Score 35; DB 106; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 3
 US-08-575-461-55
 Sequence 55, Application US/08575461
 GENERAL INFORMATION:
 APPLICANT: Lobi, Thomas J.
 APPLICANT: Cardarelli, Pina M.
 APPLICANT: Chang, Shiu-Jan
 TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 NUMBER OF SEQUENCES: 223

Correspondence Address:
 ADDRESSEE: Spensley Horn Jubas & Lubitz
 STREET: 1880 Century Park East, Fifth Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90067

Computer Readable Form:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

Current Application Data:
 APPLICATION NUMBER: US/08/575, 461
 FILING DATE: 04-JUN-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/961, 889
 FILING DATE: 04-JUN-1993
 APPLICATION NUMBER: US 07/550, 330
 FILING DATE: 09-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Bostich, June M.
 REGISTRATION NUMBER: 31, 238
 REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 FAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE: Disulfide-bond
 NAME/KEY: Disulfide-bond
 LOCATION: 1..5

US-08-575-461-55

RESULT 4
 US-08-625-695-10
 Sequence 10, Application US/08625695
 GENERAL INFORMATION:
 APPLICANT: Ruoslahti, Eeriki I.
 APPLICANT: Koivunen, Eeriki

Query Match 100.0%; Score 35; DB 9; Length 5;
 Best Local Similarity 100.0%; Pred. No. 5.5e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 5
 US-07-961-889-55
 Sequence 55, Application US/07961889
 GENERAL INFORMATION:
 APPLICANT: Bostich, June M.
 TITLE OF INVENTION: Cyclic Cell Adhesion Modulation
 NUMBER OF SEQUENCES: 223

Correspondence Address:
 ADDRESSEE: Spensley Horn Jubas & Lubitz
 STREET: 1880 Century Park East, Fifth Floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90067

Computer Readable Form:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

Current Application Data:
 APPLICATION NUMBER: US/07/961, 889
 FILING DATE: 04-JUN-1993
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/550, 330
 FILING DATE: 09-JUL-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Bostich, June M.
 REGISTRATION NUMBER: 31, 238
 REFERENCE/DOCKET NUMBER: Tanabe #7126/PD1381
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 455-5100
 FAX: (619) 455-5110
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE: Disulfide-bond
 NAME/KEY: Disulfide-bond
 LOCATION: 1..5

US-08-625-695-10

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RESULT 14
US-09-866-898-3
Sequence 3, Application US/09866898
Patent No. US20020051988A1
GENERAL INFORMATION:
APPLICANT: Gilchrist, Barbara A.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
FILE REFERENCE: BU96-09A2
CURRENT APPLICATION NUMBER: US/09/866, 89B
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/163, 095
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: PCT/US97/04966
PRIOR FILING DATE: 1997-03-28
PRIOR APPLICATION NUMBER: 08/625, 765
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 5
TYPE: PRT
FEATURE:
OTHER INFORMATION: Cyclic peptide
US-09-866-898-3

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Query Match 68.6%; Score 24; DB 9; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0;
Gaps 0;

Qy      1 CRGDC 5
       |:|
Db      1 CKGAC 5

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Search completed: September 22, 2004, 07:21:59
Job time : 125 secs

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RESULT 15
US-09-018-194-3
Sequence 3, Application US/09018194
Publication No. US2003017521A1
GENERAL INFORMATION:
APPLICANT: Gilchrist, Barbara A.
APPLICANT: Yaar, Mina
APPLICANT: Eller, Mark
TITLE OF INVENTION: METHODS OF INDUCING HAIR GROWTH AND
TITLE OF INVENTION: COLORATION
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Mililton Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,194
FILING DATE: 04-FEB-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793, 683
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10971
FILING DATE: 30-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/298, 941

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	Qy	2 RGDC 5 1 RGDC 4	2 RGDC 5 1 RGDC 4
	Db	.	.
RESULT 10			
US-10-722-075-1			
; Sequence 1, Application US/10722075			
; Publication No. US20040141922A1			
GENERAL INFORMATION:			
; APPLICANT: Nycomed Imaging AS			
; TITLE OF INVENTION: Improvements in or relating to			
; TITLE OF INVENTION: diagnostic/therapeutic			
; FILE REFERENCE: RE/KLaveness/054			
; CURRENT APPLICATION NUMBER: US/10/722.075			
; CURRENT FILING DATE: 2003-11-26			
; PRIOR APPLICATION NUMBER: US/08/960,054A			
; PRIOR FILING DATE: 1997-10-29			
; NUMBER OF SEQ ID NOS: 31			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 1			
; LENGTH: 4			
; TYPE: PRT			
; FEATURE:			
; OTHER INFORMATION: Description of Artificial Sequence			
US-10-722-075-1			
Query Match 74.3%; Score 26; DB 16; Length 4;			
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;			
Qy 2 RGDC 5 1 RGDC 4			
RESULT 11			
US-10-475-104-1			
; Sequence 1, Application US/10475104			
; Publication No. US20040171097A1			
GENERAL INFORMATION:			
; APPLICANT: Schneider-Mergener, Jens			
; APPLICANT: Schutkowsky, Mike			
; APPLICANT: Reimer, Ulf			
; APPLICANT: Dong, Liying			
; APPLICANT: Panse, Soren			
; APPLICANT: Scharn, Dirk			
; APPLICANT: Osterkamp, Frank			
; APPLICANT: Hummel, Gerd			
; APPLICANT: Jobron, Laurence			
; TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic Activity and a Device Therefor			
; FILE REFERENCE: 2018-0102			
; CURRENT APPLICATION NUMBER: US/10/475,104			
; CURRENT FILING DATE: 2003-10-17			
; PRIOR APPLICATION NUMBER: PCT/EP02/04265			
; PRIOR FILING DATE: 2002-04-17			
; NUMBER OF SEQ ID NOS: 144			
; SOFTWARE: PatentIn Version 3.2			
; SEQ ID NO 1			
; LENGTH: 4			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
US-10-475-104-1			
Query Match 74.3%; Score 26; DB 16; Length 4;			
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Indels 0; Gaps 0;			
Qy 1 CRGDC 5 1 CRGWC 5			

Best Local Similarity 80.0%; Pred. No: 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRGDC 5
Db 1 CNGDC 5

RESULT 6
US-09-765-614-B-1
Sequence 1, Application US/09765614B
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION:
TITLE OF INVENTION: diagnostic/therapeutic
FILE REFERENCE: REF/KLiveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
OTHER INFORMATION: Sequence:RGDc-Mal-PEG3400-DSPE

US-09-765-614-B-1

Query Match 74.3%; Score 26; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No: 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5
Db 1 RGDC 4

RESULT 9
US-10-179-743A-1
Sequence 1, Application US/10179743A
GENERAL INFORMATION:
APPLICANT: Schwartz, Jeffrey
Danahy, Michael P
Gawalt, Ellen S.
Schwarzauer, Jean E.
Midwood, Kim S.
Avalloni, Michael J.
APPLICANT: Carolus, Michael D.
APPLICANT: Enhanced Bonding Layers On Titanium Materials
TITLE OF INVENTION: ENHANCED BONDING LAYERS ON TITANIUM MATERIALS
FILE REFERENCE: P22.571-1 USA
CURRENT APPLICATION NUMBER: US/10/179,743A
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US 60/389,574
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/300,144
PRIOR FILING DATE: 2001-16-22
PRIOR APPLICATION NUMBER: US 09/668,080
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/155,398
PRIOR FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 08/794,833
PRIOR FILING DATE: 1997-02-04
PRIOR APPLICATION NUMBER: US 60/035,040
PRIOR FILING DATE: 1997-01-13
PRIOR APPLICATION NUMBER: US 60/028,949
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Synthetic RGDC

US-09-925-715-4

Query Match 74.3%; Score 26; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No: 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RGDC 5
Db 1 RGDC 4

RESULT 8
US-09-991-588B-1

Query Match 74.3%; Score 26; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No: 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-10-179-743A-1

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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: circular
US-09-364-97A-37

Query Match 100.0%; Score 35; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

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RESULT 2
US-09-912-609-9
Sequence 9, Application US/09912609
Publication No. US20041899A1
GENERAL INFORMATION:
APPLICANT: UNGER, EVAN C.
APPLICANT: MATSUNAGA, TERRY ONICHI
APPLICANT: RAMASWAMI, VARADARAJAN
APPLICANT: ROMANOWSKI, MAREK J.
TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
FILE REFERENCE: 5030-0001.24
CURRENT APPLICATION NUMBER: US/09/912,609
CURRENT FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 09/703,474
PRIOR FILING DATE: 2000-10-31
PRIOR APPLICATION NUMBER: 09/478,124
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 131
SEQUENCE ID NO: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-912-609-9
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Query Match 100.0%; Score 35; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

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RESULT 3
US-10-304-160-2
Sequence 2, Application US/10304160
Publication No. US2003009961A1
GENERAL INFORMATION:
APPLICANT: WICKHAM, THOMAS J
APPLICANT: KOVESDI, IMRE
APPLICANT: ROELVINK, PETRUS W
APPLICANT: BINFIELD, DAVID
APPLICANT: BROUGH, DOUGLAS E
APPLICANT: LIZONOVA, ALENA
TITLE OF INVENTION: METHOD AND COMPOSITION FOR TARGETING AN ADENOVIRAL VECTOR
FILE REFERENCE: 220148
CURRENT APPLICATION NUMBER: US/10/304,160
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: PCT/US01/17391
PRIOR APPLICATION NUMBER: US 09/631,191
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 60/208451
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Query Match 100.0%; Score 35; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5

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RESULT 4
US-09-995-388-48
Sequence 48, Application US/09995388
Publication No. US200106325A1
GENERAL INFORMATION:
APPLICANT: Carpenter, Jr., Alan P.
TITLE OF INVENTION: SIMULTANEOUS IMAGING OF CARDIAC PERFUSION AND A VITRONECTIN
FILE REFERENCE: EMS-2201
CURRENT APPLICATION NUMBER: US/09/995,388
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 60/253,324
PRIOR FILING DATE: 2000-11-27
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.2
SEQ ID NO: 48
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-09-995-388-48
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Query Match 85.7%; Score 30; DB 12; Length 5;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CNGDC 5

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RESULT 5
US-10-033-769-11
Sequence 11, Application US/10033769
Publication No. US20020094316A1
GENERAL INFORMATION:
APPLICANT: Liu, Shuang
TITLE OF INVENTION: POLYPORAL CHELANTS FOR METALLOPHARMACEUTICALS
FILE REFERENCE: EMS-2204
CURRENT APPLICATION NUMBER: US/10/033,769
CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: US 60/260,619
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 11
SEQ ID NO: 11
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-033-769-11
Query Match 85.7%; Score 30; DB 12; Length 5;
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GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 22, 2004, 07:10:50 ; Search time 124 Seconds

12.949 Million cell updates/sec
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 Perfect score: 35

Sequence: 1 CRGDC S

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 Gapop 10.0 , Gapext 0.5

Searched: 1342398 seqs, 321133274 residues

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Maximum DB seq length: 5

Post-processing: Minimum Match 0\$

Maximum Match 100\$

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16: /cgn2_6/picodata/1/pubpa/us10D_PUBCOMB.pep:*
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SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	35	100.0	5	9	US-09-765-086-8	Sequence 8, Appli
2	35	100.0	5	12	US-09-843-221-37	Sequence 37, Appli
3	35	100.0	5	14	US-10-609-217-1075	Sequence 10/5, Appli
4	30	85.7	5	12	US-10-632-388-1075	Sequence 10/5, Appli
5	30	85.7	5	12	US-10-652-244-24	Sequence 24/5, Appli
6	26	74.3	4	9	US-10-651-723-1075	Sequence 10/5, Appli
7	26	74.3	4	9	US-10-645-761-1075	Sequence 10/5, Appli
8	26	74.3	4	11	US-10-646-869-1075	Sequence 10/5, Appli
9	26	74.3	4	15	US-10-714-564A-259	Sequence 25/5, Appli
10	26	74.3	4	16	US-10-046-801-24	Sequence 3/5, Appli
11	26	74.3	4	16	US-10-475-104-1	Sequence 3/5, Appli
12	26	74.3	5	14	US-10-046-801-24	Sequence 3/5, Appli
13	25	71.4	5	16	US-10-714-564A-259	Sequence 3/5, Appli
14	24	68.6	5	9	US-09-866-998-3	Sequence 3/5, Appli
15	24	68.6	5	10	US-09-018-194-3	Sequence 3/5, Appli

ALIGNMENTS

RESULT 1
 US-09-364-597A-37
 ; Sequence 37, Application US/09364597A
 ; Patent No. US2002010130A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruoslahti, Erkki
 ; ADDRESS: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/364-597A
 ; FILING DATE: 30-JUL-1999
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/158, 001
 ; FILING DATE: 24-NOV-1993
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/286, 861
 ; FILING DATE: 04-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Kathryn
 ; REGISTRATION NUMBER: 31, 815
 ; TELECOMMUNICATION INFORMATION:
 ; REFERENCE/DOCKET NUMBER: P-LA 3419
 ; TELEPHONE: (858) 535-9001
 ; TELEX/FAX: (858) 535-8949

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The invention relates to a composition comprising a bioactive agent homogeneously dispersed in a targeted matrix (polymer and targeting ligand). Also included are a targeted matrix for use as a delivery vehicle comprising a polymer associated with a targeting ligand, enhancing the bioavailability of an agent comprising administration of the composition and treating cancer comprising administration of the novel composition. The method is useful for targeted delivery of a drug, especially in cancer therapy. The targeting ligand may be a peptide. Examples of targeting peptides are disclosed including cathepsin-D substrate peptides, peptides targeting receptors in the brain and kidney, peptides recognising fibronectin and vitronectin binding integrins, peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies, peptides targeting the angiogenic endothelium of solid tumours, tissue specific peptides (e.g. of lung, skin, pancreas, intestine, uterus, adrenal gland and retina), and cationic cancer-targeting peptides. The present sequence is a peptide targeting ligand disclosed in the invention

xx Sequence 5 AA;

Query Match	100.0%	Score	35;	DB	6;	Length	5;
Best Local Similarity	100.0%	Pred.	No.	1.4e-06;			
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	CRGDC	5				
Db	1	CRGDC	5				

Search completed: September 22, 2004, 07:50:29
Job time : 122 secs

XX
PF 27-AUG-1998; 98US-00141127.
XX
PR 21-MAY-1992; 92US-00886752.
XX
PR 21-MAY-1993; 93WO-US004194.
XX
PR 05-JAN-1995; 95US-00335832.
XX
PA (DIAT-) DIATIDE INC.
XX
PI Lister-James J, Dean RT;
XX
DR WPI; 2000-498061/44.
XX
PT Composition comprises technetium-99m and polyamide reagent which binds to thrombi, useful as scintigraphic imaging agent for imaging sites of thrombus formation in vivo.
XX
PS Example 2; Col 15-16; 27pp; English.
XX
CC The present sequence is that of a peptide that acts as a ligand for the GPIb/IIIA receptor. The invention relates to radiolabeled reagents that are scintigraphic imaging agents for imaging sites of thrombus formation in vivo. The reagents each comprise a specific binding compound, such as the present peptide, that is capable of binding to at least 1 component of a thrombus, and which is covalently linked to a radiolabel-binding moiety. A method for using such a reagent labeled with technetium-99m to image a thrombus site in a mammalian body is claimed
XX
SQ Sequence 5 AA;
- Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Length 5; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CRGDC 5
Db 1 CRGDC 5
RESULT 17
AAE17982 ID AAE17982 standard; peptide; 5 AA.
XX
AC AAE17982;
XX
DT 07-MAY-2002 (first entry)
DE Human ligand #2 attached to an adenoviral vector.
XX
KW Human; adenoviral coat protein; non-native ligand; cell-surface receptor; KW therapy; anti-tumour agent; tumour necrosis factor; cancer; brain; lung; KW ovary; breast; prostate.
XX
OS Homo sapiens.
XX
PN WO200192549-A2.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US017391.
XX
PR 31-MAY-2000; 2000US-0208451P.
PR 02-AUG-2000; 2000US-00631191.
XX
PA (GENVC) GENVEC INC.
XX
PI Wickham TJ, Kovacs I, Roelvink PW, Einfeld D, Brough DE;
PI Lizonova A;
XX
DR WPI; 2002-147620/19.
XX
PT Adenoviral coat protein which permits production of adenoviral vectors
PT that bind and infect host cells not naturally infected by adenovirus,
PT

XX
PT comprises various non-native ligands.
XX
PS Claim 4; Page 40; 45pp; English.

XX
The invention relates to adenoviral coat proteins comprising various non-native ligands. The invention provides a method of controlled gene expression utilising selectively replicating competence and also a method and a composition for targeting an adenoviral vector. A system comprising a cell having a non-native cell-surface receptor, and a virus having a non-native ligand which binds the non-native cell-surface receptor of the cell is useful for propagating a virus and also for assaying gene function. The system is also useful for isolating a nucleic acid encoding a product comprising a desired property. Further, the system is useful for identifying functionally related coding sequences. Adenoviral vector comprising a non-native nucleic acid encoding a therapeutic agent, such as anti-tumour agent, preferably tumour necrosis factor and a second non-native nucleic acid encoding an agent that facilitates imaging and a targeting agent is useful for treating an animal. The therapeutic agent can be used to treat cancer of the brain, lung, ovary, breast and prostate. The present sequence is human non-native ligand attached to an adenoviral vector.

XX
SQ Sequence 5 AA;
Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 1.4e-06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
Qy 1 CRGDC 5
ID ABU59650 standard; peptide; 5 AA.
XX
Db 1 CRGDC 5
AC ABU59650;
XX
DT 22-APR-2003 (first entry)
XX
DE Fibronectin-binding integrin alpha5-beta1 targeting peptide #11.
XX
KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytosatic; cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor; fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium; tumour; cationic cancer-targeting Peptide.
XX
SYNTHETIC
XX
OS US2002041898-A1.
XX
PD 11-APR-2002.
XX
PF 25-JUL-2001; 2001US-00912609.
XX
PR 05-JAN-2000; 2000US-00478124.
XX
PR 31-OCT-2000; 2000US-00703474.
XX
PA (UNGEB) UNGER, B. C.
PA (MATS) MATSUNAGA, T. O.
PA (RAMA) RAMASWAMI, V.
PA (ROMA) ROMANOWSKI, M. J.
XX
PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;
XX
DR WPI; 2003-208921/20.
XX
PT Targeted delivery system comprising a bioactive agent homogeneously dispersed in a targeted matrix is especially useful in cancer therapy.
XX
PS Claim 42; Page 38; 46pp; English.

CC inexpensively synthesised
 XX SQ Sequence 5 AA;

Query Match 100.0%; Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

KW Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 GPIIb/IIIa receptor; cyclic peptide ligand.

OS Synthetic.
 XX PN US5968476-A.
 XX PD 19-OCT-1999.
 XX AC AAY54976;
 XX DT 15-FEB-2000 (first entry)
 XX DB Peptide ligand for fibrin polymerisation site.

RESULT 14
 ADE25491 ID ADB25491 standard; peptide; 5 AA.
 XX AC ADB25491;
 XX DT 29-JAN-2004 (first entry)
 XX DE Tc-99m labelled peptide #49.
 XX KW Thrombus imaging agent; GPIIb/IIIa receptor; thrombus.
 OS Synthetic.
 XX PN US5888474-A.
 XX PD 30-MAR-1999.
 XX PP 07-JUN-1995; 95US-00478725.
 XX PR 08-FEB-1991; 91US-00653012.
 XX PR 27-NOV-1991; 91US-00807062.
 XX PR 21-MAY-1992; 92US-00886752.
 XX PR 22-JUN-1994; 94US-00264176.
 XX PR 11-JUL-1994; 94US-0027274.
 XX PR 07-JUN-1995; 95US-00480951.
 XX PA (DIAT-) DIATIDE INC.
 XX PI Dean RT, Lister-James J;
 XX DR WPI; 2000-021733/02.

XX PN US5968476-A.
 XX PR A complex used for thrombus imaging comprises technetium-99m complexed
 with a Peptide ligand for GPIIb/IIIa receptor.
 XX PS Example 2; Col 13-14; 18pp; English.
 XX PR A complex used for thrombus imaging comprises a peptide ligand for the fibrin polymerisation
 site. The invention relates to a complex (A) for thrombus imaging
 comprises technetium-99m (Tc-99m) complexed with a reagent comprising a
 peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding
 moiety covalently bound to (P). (P) is selected from a linear peptide
 ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence
 (arginine-glycine-aspartate), a peptide ligand for a polymerisation site
 of Fibrin, and a cyclic peptide ligand for the GPIb/IIIa receptor. The
 thrombus imaging reagents provided by the present invention can be used
 for visualising thrombi in a mammalian body when Tc-99m is labelled
 XX SQ Sequence 5 AA;

Query Match 100.0%; Score 35; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRGDC 5
 Db 1 CRGDC 5

KW Thrombus; imaging; radioimaging; thrombosis; thromboembolism; embolism;
 KW diagnosis; technetium-99m; GPIIb/IIIa receptor ligand.

OS Synthetic.
 XX PN US6083481-A.
 XX PD 04-JUL-2000.

RESULT 15
 AAY54976

PA (DIATIDE INC.
 PA (YMSC-) UNIV SOUTHERN CALIFORNIA.
 XX Markland FS, Bush IR, Swenson S, Flores Sanchez E;
 PI WPI; 1998-333336/29.

XX New thrombolytic agents - comprise thrombolytic proteinase covalently
 PT linked to targetting compound for binding to component of thrombus.
 XX
 PT Claim 10; Page 65; 79pp; English.

XX The invention relates to new thrombolytic agents which comprise a
 CC thrombolytic proteinase covalently linked to a targetting compound
 CC capable of specifically binding to a component of a thrombus. The
 CC thrombolytic agents can be used for eliminating thrombi in vivo in, e.g.
 CC myocardial infarction, cerebral ischaemia, deep vein thrombosis or
 CC pulmonary embolism. A labelled form of the thrombolytic agent can also be
 CC used to image thrombi for diagnostic purposes. The thrombolytic agents
 CC are specifically targeted to thrombus sites in vivo and have minimal
 CC haemorrhagic side effects and side effects related to non-specific
 CC proteolysis. The present sequence represents a specifically claimed
 CC targetting peptide. (Updated on 25-MAR-2003 to correct PI Field.)

XX Sequence 5 AA;

PS Query Match 100.0%; Score 35; DB 2; Length 5;
 PS Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 PS Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PS Qy 1 CRGDC 5
 PS Db 1 CRGDC 5

PS RESULT 13
 PS ID AAY21570 standard; peptide; 5 AA.
 PS XX AAY21570;
 PS AC XX DT 09-AUG-1999 (first entry)
 PS DE XX DB Integrin-binding peptide.
 PS XX KW Integrin; fibronectin; vitronectin; extracellular matrix protein;
 PS KW metastatic; fibronectin adhesion; alphasbeta1 integrin.
 PS OS XX Synthetic.
 PS PN XX US5912234-A.
 PS PD XX 15-JUN-1999.
 PS PP XX 03-APR-1996; 96US-00625695.
 PS PR XX 27-SEP-1993; 93US-00127422.
 PS PR XX 11-MAR-1994; 94US-00212186.
 PS PA XX (LJOL-) LA JOLLA CANCER RES FOUND.
 PS PI XX Koivunen E, Ruoslahti E;
 PS DR XX WPI; 1999-35721/30.
 PS PT XX Integrin-binding peptides has specific binding specificity for
 PS CC fibronectin and vitronectin binding integrins.
 PS Disclosure; Col 15; 16pp; English.

XX The invention relates to peptides having specific binding specificity for
 CC fibronectin-binding and vitronectin-binding integrins, and in particular
 CC for alpha5beta1 integrin. The peptides can be used in a method of
 CC preventing integrin-mediated attachment to an extracellular matrix
 CC protein, fibronectin, or vitronectin which comprises (a) contacting the
 CC peptides with a soluble peptide selected from the sequences shown in
 CC AAY21561, AAY21563 and AAY21566; or (b) contacting the cells with a
 CC soluble peptide comprising the sequence -NGR- selected from the sequences
 CC shown in AAY21564, AAY21566 or AAY21573; or (c) contacting with a soluble
 CC peptide shown in AAY21571. The peptides are useful for inhibiting
 CC metastatic process with which fibronectin adhesion is associated and also
 CC for inhibiting alpha v beta 1-mediated cell attachment to fibronectin,
 CC and alpha v beta 5-mediated cell attachment to vitronectin. The peptides
 CC are also useful for promoting attachment of integrin expressing cells to
 CC a surface or artificial cell matrix. The peptides can be easily and
 XX

PA (DIATIDE INC.
 XX Lister-James J, Dean RT;
 PI WPI; 1998-239148/21.

XX Reagent useful for preparing thrombus imaging agent - comprises peptide
 PT covalently linked to technetium binding moiety which is technetium
 PT labelled and binds to thrombus component.
 XX

RESULT 9
 ID AAW03492 standard; peptide; 5 AA.
 XX
 AC AAW03492;
 XX
 DT 25-MAR-2003 (revised)
 24-OCT-1996 (first entry)
 XX
 Alpha(5)-Beta(1) integrin binding peptide 10.
 XX
 KW Synthetic; fibronectin; integrin; binding motif; adhesion;
 extracellular matrix protein; tumour metastasis.
 XX
 OS Synthetic.
 XX
 PN US5536814-A.
 XX
 PD 16-JUL-1996.
 XX
 FF 11-MAR-1994; 94US-00212186.
 XX
 PR 27-SEP-1993; 93US-00127422.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Koivunen E; Ruoslahti E;
 XX
 DR WPI; 1996-341556/34.
 XX
 PT Synthetic integrin-binding peptide(s) - useful for inhibiting tumour
 metastasis, etc.
 XX
 Disclosure: Col 2; 16pp; English.
 XX
 Peptides AAW03493-508 are examples of synthetic peptides generated to
 bind to the fibronectin/vitronectin-binding integrin alpha(5)beta(1).
 They are synthesised to contain the alpha(5)beta(1)-integrin peptide
 binding motifs: DGR, NGR or RGD. The peptides interfere with the binding
 of fibronectin and vitronectin to this integrin and thus may be used to
 block integrin-mediated cell adhesion to extracellular matrix proteins,
 esp. to inhibit tumour metastasis. (Updated on 25-MAR-2003 to correct PPT
 field.)
 XX
 Sequence 5 AA:
 SQ Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db Query Match Score 35; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 ID AAW8499 standard; peptide; 5 AA.
 XX
 AC AAW8499;
 XX
 DT 18-AUG-1998 (first entry)
 XX
 DE Integrin receptor antagonist peptide 38.
 XX
 KW Integrin receptor antagonist; cell adhesion modulator; leukocyte;
 extracellular matrix; fibronectin; ARDS; thrombosis; inflammation.
 XX
 OS Synthetic.
 XX
 FH Key Disulfide-bond Location/Qualifiers 1..5
 FT

XX
 PN US5721210-A.
 XX
 PD 24-FEB-1998.
 XX
 PP 07-JUN-1995; 95US-00485019.
 XX
 PR 09-JUL-1990; 90US-00550330.
 PR 09-JUL-1991; 91WO-US004862.
 PR 04-JUN-1993; 93US-00961889.
 XX
 PA (TANABE SEIYAKU CO.
 XX
 PI Cardarelli PM, Lohr TJ, Chiang S;
 XX
 DR WPI; 1998-16842/15.
 XX
 PT New cyclic peptide(s) and peptidomimetic compounds - are integrin
 receptor antagonists useful in modulating cell adhesion.
 XX
 PS Example 9; Col 42; 32pp; English.
 XX
 The present sequence represents a synthetic peptide which acts as an
 antagonist to integrin receptors. The invention provides various
 synthetic peptides which act as cell adhesion modulators because they
 mimic extra-cellular matrix ligands or other cell adhesion ligands that
 bind to receptors such as integrin receptors, including fibronectin,
 laminin, LFA-1, MAC-1, p150,95, vitronectin and gp130/110a receptors.
 Some of the peptides contain the amino acid sequence Arg-Gly-Asp (RGD).
 Others contain non-RGD sequences, for e.g. RCD sequences and reverse
 orientation forms of amino acid residues. The synthetic peptides are
 useful in modulating cell adhesion, including adhesion related to
 fibronectin, as well as leukocyte adhesion to endothelial cells. They are
 also claimed to be useful in the study, diagnosis, treatment or
 prevention of diseases which relate to cell adhesion, e.g. adult
 respiratory distress syndrome (ARDS), thrombosis and inflammatory
 conditions
 XX
 Sequence 5 AA:
 SQ Query Match Score 100.0%; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db Query Match Score 100.0%; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 ID AAW64952 standard; peptide; 5 AA.
 XX
 AC AAW64952;
 XX
 DT 25-MAR-2003 (revised)
 23-SEP-1998 (first entry)
 XX
 DE Targetting peptide #45 useful as component of thrombolytic agent.
 XX
 KW Thrombolytic agent; thromolytic proteinase; blood clot; fibrin;
 thrombus; antithrombotic activity.
 XX
 OS Synthetic.
 XX
 PN WO9824917-A1.
 XX
 PD 11-JUN-1998.
 XX
 PR 02-DEC-1997; 97WO-US021918.
 XX
 PR 02-DEC-1996; 96US-00753781.

XX WPI; 1992-313678/38.
 XX New synthetic Peptide lipids or salts - useful as cell migration
 inhibitors, cell adhesion membranes and cell culture bodies.
 XX Disclosure; Page 3; 9pp; Japanese.

The Peptide sequence is an example of a highly generic sequence contd:
 CC the RGD motif. Compounds contg. these lipid peptides are useful as cell
 migration inhibitors in cell adhesion membranes or cell culture bodies.
 See also AAR29048-54.

SQ Sequence 5 AA;

Query Match	100.0%	Score	35;	DB	2;	Length	5;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;				
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 8
 AAR79093 ID AAR79093 standard; peptide; 5 AA.
 XX AC AAR79093;
 XX DT 24-JAN-1996 (first entry)
 XX DB Alpha5/beta1 integrin binding peptide #20.

XX High affinity, integrin binding peptide; alpha5/beta1; alphav/beta5;
 KW alphav/beta3; RGD; stable configuration; wound healing;
 KW osteoclast attachment; bone; angiogenesis; metastasis; tumour;
 KW smooth muscle cell migration.

SQ Sequence 5 AA;

Query Match	100.0%	Score	35;	DB	2;	Length	5;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;				
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 CRGDC 5
 Db 1 CRGDC 5

RESULT 7
 AAR69325 ID AAR69325 standard; peptide; 5 AA.
 XX AC AAR69325;
 XX DT 25-MAR-2003 (revised)
 XX DT 25-JUN-1995 (first entry)
 XX DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.
 XX Scintigraphy; thrombus; thrombi; imaging; specific binding;
 KW technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.
 XX Synthetic.

XX WO9323085-A1.
 XX 25-NOV-1993.
 XX 21-MAY-1993; 93WO-US004794.
 XX PR 21-MAY-1992; 92US-00886752.
 XX (DIAT-) DIATECH INC.
 XX Dean RT, Lister-James J;
 XX DR 1993-386229/48.
 XX Reagent for scintigraphic imaging of thrombi with 99m technetium -
 PT comprises synthetic peptide which binds to thrombus covalently coupled to
 PT metal binding gp., rapidly cleared from blood and tissue.
 XX Claim 41; Page 46; 61pp; English.

The invention relates to reagents for scintigraphic imaging of a thrombus
 CC in-vivo, comprising (A) a specific binding compound capable of binding to
 CC at least one component of a thrombus, covalently linked to (B) a
 CC technetium-99m-binding moiety. Specific peptides constituting the
 CC reagents are claimed as new. The present peptide is one such peptide.
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 5 AA;

Query Match	100.0%	Score	35;	DB	2;	Length	5;
Best Local Similarity	100.0%	Pred. No.	1.4e+06;				
Matches	5;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						

Qy 1 CRGDC 5
 Db 1 CRGDC 5

Qy	1 CRGDC 5 1 CRGDC 5	Query Match Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1 CRGDC 5
Db	AAR10415 AC AAR10415; XX	RESULT 2 AAR10415 ID AAR10415 standard; protein; 5 AA. XX XX DT 10-APR-1991 (first entry) XX DE Fibrinogen receptor antagonising peptide (III). XX KW Fibrinogen receptor antagonist; platelet aggregation; thrombosis; myocardial infarction. XX FT Disulfide-bond 1..5 OS Synthetic. XX PN EP410537-A. XX PH 30-JAN-1991. XX PF 23-JUL-1990; 90EP-00202015. XX PR 28-JUL-1989; 89US-00386534. XX PA (MERI) MERCK & CO INC. XX PI Nutt RF, Brady SF, Veber DF; XX DR WPI; 1991-030928/05. XX PT New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery. XX PS Claim 4; Page 10; 10pp; English. XX CC To residue Cys5 is attached OH. The peptide is prep. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of coronary arteries and after angioplasty or reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or antiocoagulants. See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410541, and EP-410767 XX SQ Sequence 5 AA;	RESULT 3 AAR10414 ID AAR10414 standard; protein; 5 AA. XX AC AAR10414; XX DT 10-APR-1991 (first entry) XX DE Fibrinogen receptor antagonising peptide (II). XX KW Fibrinogen receptor antagonist; platelet aggregation; thrombosis; myocardial infarction. XX FT Disulfide-bond 1..5 OS Synthetic. XX PN EP410537-A. XX PH 30-JAN-1991. XX PF 23-JUL-1990; 90EP-00202015. XX PR 28-JUL-1989; 89US-00386534. XX PA (MERI) MERCK & CO INC. XX PI Nutt RF, Brady SF, Veber DF; XX DR WPI; 1991-030928/05. XX PT New fibrinogen receptor antagonising peptide cpds. - used to inhibit blood platelet aggregation during surgery on peripheral arteries and in cardiovascular surgery. XX PS Claim 4; Page 10; 10pp; English. XX CC To residue Cys5 is attached OH. The peptide is prep. using standard methods of solid phase synthesis and is one of 17 pref. examples of a highly generic formula. The peptide is used to inhibit fibrinogen-induced platelet aggregation and is partic. useful because it does not significantly deplete the platelet count. It has a relatively short duration of activity and is thus useful where prevention of platelet aggregation over a short period of time is desirable, e.g. in surgery of coronary arteries and after angioplasty or reocclusion either during and after thrombolytic therapy, or after angioplasty of coronary and other arteries and after coronary artery by-pass procedures, or to prevent myocardial infarction. It may be combined with thrombolytic agents, e.g. plasminogen activators or streptokinase, or antiocoagulants. See also AAR10413-18 and EP-410537, EP-410539, EP-410540, EP-410541, and EP-410541, and EP-410767 XX SQ Sequence 5 AA;	RESULT 4 AAR10418 ID AAR10418 standard; protein; 5 AA. XX AC AAR10418;
Qy	1 CRGDC 5 	Query Match Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1 CRGDC 5 1 CRGDC 5 1 CRGDC 5
SQ	Sequence 5 AA;	Query Match Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	1 CRGDC 5 1 CRGDC 5 1 CRGDC 5

Result No.	Score	Query	Match	Length	DB ID	Description
1	35	100.0	5	2	AAR11587	Aar11587 Fibrino
2	35	100.0	5	2	AAR10415	Aar10415 Fibrinoge
3	35	100.0	5	2	AAR10414	Aar10414 Fibrinoge
4	35	100.0	5	2	AAR10418	Aar10418 Fibrinoge
5	35	100.0	5	2	AAR27031	Aar27031 Peptide 1
6	35	100.0	5	2	AAR29052	Aar29052 Peptide 1
7	35	100.0	5	2	AAR69325	Aar69325 GP IIB/III
8	35	100.0	5	2	AAR79093	Aar79093 Alpha5/be
9	35	100.0	5	2	Aaw03492	Aaw03492 Alpha(5)-
10	35	100.0	5	2	Aaw48499	Aaw48499 Integrin
11	35	100.0	5	2	Aaw64352	Aaw64352 Targetin
12	35	100.0	5	2	Aaw50594	Aaw50594 GPIIb/III
13	35	100.0	5	2	AAY21570	Aay21570 Integrin-
14	35	100.0	5	2	ADE25491	Ade25491 TC-99m la
15	35	100.0	5	2	AAY54976	Aay54976 Peptide 1
16	35	100.0	5	3	AAY5465	Aay5465 GPIIb/III
17	35	100.0	5	5	AAB17982	Aab17982 Human lig
18	19	100.0	5	6	ABU59650	Abu59650 Fibronect
19	32	91.4	5	2	AAY16250	Aay1625 Snake ven
20	30	85.7	5	3	AAO22876	Aao22876 Angiogeni
21	30	83.7	5	4	AAB97087	Aab97087 Integrin-
22	30	85.7	5	5	ABP54052	ABP54052 Alpha-v-b
23	30	85.7	5	5	ABG70730	Abg70730 avB5 bind
24	30	85.7	5	5	AAU79139	Aau79139 Synthetic
25	30	85.7	5	5	AAG78428	Aag78428 Cyclic pe

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 22, 2004, 07:48:21 ; Search time 121 Seconds
Title: US-09-912-609-9
Perfect score: 35
Sequence: 1 CRGDC 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 5
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ALIGNMENTS

RESULT 1
ID AAR11587 standard; protein; 5 AA.

AC AAR11587;
XX DT 12-JUN-1991 (first entry)
XX DE Fibrinogen receptor antagonist #4.
XX KW fibrinogen receptor antagonist; thrombosis; fibrinogen; IIB/IIIa receptor.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Disulfide-bond 1..5
FT Modified-site 2
XX /label= Arg (phenyl)

XX EP422938-A.

XX PD 17-APR-1991.
XX PP 11-OCT-1990;
XX PA 13-OCT-1989;
XX PA (MERCK & CO INC.
XX PI Nutt RF, Brady ST, Veber KP, Duggan MF;
XX XX Disclosure: Page 7, 16pp; English.
XX DR WPI: 1991-11423/16.
XX PT Polypeptide fibrinogen receptor antagonists - used to prevent thrombosis,
PT e.g. during cardiovascular surgery.

XX CC Cys at position 1 carries an acetyl group. The peptide inhibits binding
CC of fibrinogen to the platelet membrane glycoprotein complex IIB/IIIa
CC receptor. It may be used to prevent post-operative thrombosis,
CC thromboembolism and reocclusion, platelet adhesion in extracorporeal
CC blood circulation systems and to prevent myocardial infarction. See also
CC ARI11584-6 and ARI11588-R11594
XX SQ Sequence 5 AA;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	35	100.0	5	2	AAR11587	Aar11587 Fibrino
2	35	100.0	5	2	AAR10415	Aar10415 Fibrinoge
3	35	100.0	5	2	AAR10414	Aar10414 Fibrinoge
4	35	100.0	5	2	AAR10418	Aar10418 Fibrinoge
5	35	100.0	5	2	AAR27031	Aar27031 Peptide 1
6	35	100.0	5	2	AAR29052	Aar29052 Peptide 1
7	35	100.0	5	2	AAR69325	Aar69325 GP IIB/III
8	35	100.0	5	2	AAR79093	Aar79093 Alpha5/be
9	35	100.0	5	2	Aaw03492	Aaw03492 Alpha(5)-
10	35	100.0	5	2	Aaw48499	Aaw48499 Integrin
11	35	100.0	5	2	Aaw64352	Aaw64352 Targetin
12	35	100.0	5	2	Aaw50594	Aaw50594 GPIIb/III
13	35	100.0	5	2	AAY21570	Aay21570 Integrin-
14	35	100.0	5	2	ADE25491	Ade25491 TC-99m la
15	35	100.0	5	3	AAY54976	Aay54976 Peptide 1
16	35	100.0	5	3	AAY5465	Aay5465 GPIIb/III
17	35	100.0	5	5	AAB17982	Aab17982 Human lig
18	19	100.0	5	6	ABU59650	Abu59650 Fibronect
19	32	91.4	5	2	AAY16250	Aay1625 Snake ven
20	30	85.7	5	3	AAO22876	Aao22876 Angiogeni
21	30	83.7	5	4	AAB97087	Aab97087 Integrin-
22	30	85.7	5	5	ABP54052	ABP54052 Alpha-v-b
23	30	85.7	5	5	ABG70730	Abg70730 avB5 bind
24	30	85.7	5	5	AUU79139	Auu79139 Synthetic
25	30	85.7	5	5	AAG78428	Aag78428 Cyclic pe

OC Gallus.
 OC NCBI_TaxID=9031;
 RN
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Brain;
 RX PubMed=613771;
 RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 "A novel active pentapeptide from chicken brain identified by
 antibodies to FMRFamide.";
 RL Nature 305:328-330 (1983).
 CC -; FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
 CC -; SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 DR GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 645 MW; 694073767400000 CRC64;

Query Match 14.3%; Score 5; DB 13; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 Db 4 R 4

RESULT 4
 ID P83568 PRELIMINARY; PRT; 4 AA.
 AC DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DE Pheromone peptide ILME.
 OS Sepia officinalis (Common cuttlefish).
 OC Bivalvia; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea;
 OC Decapodiformes; Sepioidea; Sepidae; Sepia.
 NCBI_TAXID=6610;
 RN
 RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
 TISSUE=EGG;
 RA Zatyrny C., Gagnon J., Boucaud-Camou E., Henry J.;
 RT "a waterborne pheromonal peptide released by the eggs of Sepia
 officinalis.";
 RL Biochem. Biophys. Res. Commun. 275:217-222 (2000).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=EGG;
 RX PubMed=11207899;
 RA Zatyrny C., Marvin L., Gagnon J., Henry J.;
 RT "Fertilization in Sepia officinalis: the first mollusk sperm-
 attracting peptide.";
 RT Biochem. Biophys. Res. Commun. 296:1186-1193 (2002).
 CC -; SUBCELLULAR LOCATION: SECRETED.
 CC -; TISSUE SPECIFICITY: FOLLICLE, FULLY GROWN OCYCTE AND EGG (EC2).
 CC -; MASS SPECTROMETRY: MW=505.4; METHOD=MALDI.
 DR Pheromone. Pheromone activity; IEA.
 SQ SEQUENCE 4 AA; 505 MW; 6B1697203000000 CRC64;

Query Match 5.7%; Score 2; DB 5; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 D 4
 Db 4 E 4

RESULT 5
 ID Q08433 PRELIMINARY; PRT; 4 AA.
 AC DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Bilirubin UDP-glucuronosyltransferase (Fragment).
 OS Rattus sp.
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TAXID=10118;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gunn;
 RX MEDLINE=9128278; PubMed=1840486;
 RA Sato H., Aono S., Kashiyama S., Koiwai O.;
 RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
 hyperbilirubinemic Gunn rat.";
 RT Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).
 DR EMBL: S38636; PDB:1959.1; -.
 DR GO:00016740; F:transferase activity; IEA.
 KW Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 4 AA; 473 MW; 633732C4200000000 CRC64;

Query Match 5.7%; Score 2; DB 11; Length 4;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 Db 4 K 4

RESULT 6
 ID Q99007 PRELIMINARY; PRT; 5 AA.
 AC DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha amylase (Fragment).
 GN AMYL_GENE.
 OS Hordeum vulgare (Barley).
 OC Bukaryota; Viridiplantae; Streptophytina; Embryophytina;
 OC Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 NCBI_TAXID=4513;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91329704; PubMed=1831055;
 RA Jacobsen J.V., Close T.J.;
 RT "Control of transient expression of chimaeric genes by gibberellic
 acid and abscisic acid in protoplasts prepared from mature barley
 aleurone layers";
 RT Plant Mol. Biol. 16:713-721 (1991).
 DR EMBL: X54643; PDB:19A3B455.1; -.
 DR NON_TER 5 5
 SQ SEQUENCE 5 AA; 600 MW; 61B3344DD6F00000 CRC64;

Query Match 5.7%; Score 2; DB 10; Length 5;
 Best Local Similarity 0.0%; Pred. No. 1e+06;
 Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 R 2
 Db 4 K 4

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CC	EMBL; M21922; -; NOT ANNOTATED CDS.	OC	Pelodryadinae; Litoria.
DR	PIR; I40697; -	OX	NCBI_TaxID=104895;
DR	InterPro; IPR005814; Aminotransf	RN	SEQUENCE, AND MASS SPECTROMETRY.
DR	PROSITE; PS00600; AA_TRANSFER CLASS 3; PARTIAL.	RP	TISSUE=Skin secretion;
KW	Biotin biosynthesis; Transf erase; Aminotransferase;	RC	Steinborner S.T.; Wabnitz P.A.; Waugh R.J.; Bowie J.H.; Gao C.;
KW	Pyridoxal phosphate.	RA	Tyler M.J.; Wallace J.C.;
FT	NON_TER 5 5	RT	"The structure of new Peptides from the Australin red tree frog 'Litoria rubella.' The skin peptide profile as a probe for the study of evolutionary trends of amphibians."
SQ	SEQUENCE 5 AA; 582 MW; 6AAB1B1A6F0000 CRC64;	RT	RT
	Query Match 17.1%; Score 6; DB 1; Length 5;	RL	Aust. J. Chem. 49:955-963 (1996).
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	CC	-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
	Matches 1; Conservative 0; N mismatches 0; Indels 0;	CC	activity.
Qy	4 D 4	CC	-!- SUBCELLULAR LOCATION: Secreted.
Db	4 D 4	CC	-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
	Query Match 17.1%; Score 6; DB 1; Length 5;	CC	-!- MASS SPECTROMETRY: MW=538; METHOD=FAB.
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	KW	Amphibian defense peptide.
	Matches 1; Conservative 0; N mismatches 0; Indels 0;	SQ	SEQUENCE 5 AA; 598 MW; 6DD9C9CAB2A00000 CRC64;
	Query Match 17.1%; Score 6; DB 1; Length 5;	Qy	4 D 4
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	Db	2 D 2
	Matches 1; Conservative 0; N mismatches 0; Indels 0;		
RESULT 13		RESULT 15	
PAP2_PARMA	PAP2_PARMA STANDARD; PRT; 5 AA.	RE32_LITRU	RE32_LITRU STANDARD; PRT; 5 AA.
AC	P81854;	ID	RE32_LITRU STANDARD; PRT; 5 AA.
DT	30-MAY-2000 (Rel. 39, Created)	ID	P82073;
DT	30-MAY-2000 (Rel. 39, Last sequence update)	AC	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last annotation update)	AC	28-FEB-2003 (Rel. 41, Last sequence update)
DE	Pardaxin II (PXXII) (Fragment)	DB	10-OCT-2003 (Rel. 42, Last annotation update)
OS	Pardachirus marmoratus (Red sea moses sole).	OS	Rubellidin 3.2.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;	OS	Litoria rubella (Desert tree frog).
OC	Actinopterygii; Neopterygii; Teleostei; Euteleosteii; Neoteleosteii;	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC	Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;	OC	Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC	Soleoidei; Soleidae; Pardachiridae.	OC	Pelodryadinae; Litoria.
OX	NCBI_TaxID=31087;	OX	NCBI_TaxID=104895;
RN	[1]	RN	[1]
RP	SEQUENCE.	RP	SEQUENCE.
RC	TISSUE=Skin secretion;	RC	TISSUE=Skin secretion;
RC	MEDLINE=81057369; Pubmed=3782138;	RA	Wabnitz P.A.; Bowie J.H.; Tyler M.J.; Wallace J.C.;
RA	RAZKOVIC P.; PRIMOR N.; LOW L.M.;	RA	"Peptides from the skin glands of the Australian buzzing tree frog Litoria electrica. Comparison with the skin peptides from Litoria rubella." Aust. J. Chem. 52:639-645 (1999).
RT	RT	RT	-!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
RT	RT	CC	activity.
RT	RT	CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	CC	CC	-!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC	CC	CC	-!- AMPHIBIAN DEFENSE PEPTIDE.
CC	CC	KW	SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
CC	CC	Qy	3 G 3
CC	CC	Db	1 G 1
FT	NON_TER 5 5	Query Match 17.1%; Score 6; DB 1; Length 5;	CC
SQ	SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	CC
	Query Match 17.1%; Score 6; DB 1; Length 5;	Matches 1; Conservative 0; N mismatches 0; Indels 0;	CC
	Best Local Similarity 100.0%; Pred. No. 1.4e+05;	Ox	SEQUENCE 5 AA; 570 MW; 71A9C9C862A00000 CRC64;
	Matches 1; Conservative 0; N mismatches 0; Indels 0;	Qy	3 G 3
	Query Match 17.1%; Score 6; DB 1; Length 5;	Db	2 G 2
RESULT 14		RESULT 15	
RE11_LITRU	RE11_LITRU STANDARD; PRT; 5 AA.	RE11_LITRU	RE11_LITRU STANDARD; PRT; 5 AA.
AC	P82070;	ID	P82070;
DT	28-FEB-2003 (Rel. 41, Created)	AC	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)	AC	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Rubellidin 1.1.	DE	Litoria rubella (Desert tree frog).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;	OC	Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;

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Job time : 23 secs

DE Rosinophilic peptides.
 OS Homo sapiens (Human);
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Metazoa; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 SEQUENCE
 MEDLINE=76078412; PubMed=1060093;
 Goetzl E.J.; Austen K.F.;
 "Purification and synthesis of eosinophilic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor of anaphylaxis.",
 Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127 (1975).
 RL [1]
 CC !- MISCELLANEOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimulation of the hexose monophosphate shunt.
 CC GO: GO:0006935; P: chemotaxis; IDA.
 DR GO: GO:0006955; P: immune response; IDA.
 PT VARIANT 1 1 V->A (IN OTHER PEPTIDE). /FT1d=AR_005201.
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;
 QUERY Match 17.1%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 2 G 2
 RESULT 10
 OCP3 OCTMI
 ID OCP3_OCTMI STANDARD PRT 4 AA.
 AC P58649;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Cardioactive peptides Ocp-3/Ocp-4.
 OS Octopus minor (Octopus).
 OC Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoeloidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=89766;
 RN [1]
 SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
 TISSUE-BRAIN;
 MEDLINE=20336815; PubMed=1076044;
 RA Iwakoshi E., Hisada M., Manakata H.;
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.",
 RL Peptides 21:623-630(2000).
 CC !- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less active than Ocp-3.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
 CC -!- MASS_SPECTROMETRY: MW=395.2; METHOD=ALDI.
 KW Hormone; D-amino acid.
 PT MOD RES 2 2 D-SERINE (IN OCP-4).
 SQ SEQUENCE 4 AA; 463 MW; 6AB365BB10000000 CRC64;
 QUERY Match 17.1%; Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 1 G 1
 RESULT 11

AL14 CARMA
 ID AL14_CARMA STANDARD PRT; 5 AA.
 AC P81817;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DB Carcinustatin 14.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Bivalacustraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Subbrachyura; Portunoidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 SEQUENCE.
 RC TISSUE-Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=461295;
 RA Duke H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab *Carcinus maenas*." Eur. J. Biochem. 250:727-734(1997).
 RL !- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC !- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 PT MOD RES 5 5 AMIDATION (POTENTIAL).
 SQ SEQUENCE 5 AA; 566 MW; 672879DAB300000 CRC64;
 Query Match 17.1%; Score 6; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 4 G 4
 RESULT 12
 BIOA CITFR
 ID BIOA_CITFR STANDARD PRT; 5 AA.
 AC P13071;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DE Adenosylmethionine-8-amino-7-oxononanoate amidotransferase (EC 2.6.1.62) ('7,8-diamino-pelargonic acid amidotransferase) (DAPA amino transferase) (Fragment).
 DB BIOA.
 OC Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=89006280; PubMed=2971595;
 RA Shiu D., Campbell A.;
 RT "Transcriptional regulation and gene arrangement of *Escherichia coli*, *Citrobacter freundii* and *Salmonella typhimurium* biotin operons.". ;
 RL Gene 67:203-211(1988).
 CC !- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-oxononanoate = S-adenosyl-4-methylthio-2-oxobutanate + 7,8-diaminonoanoate.
 CC !- COFACTOR: Pyridoxal phosphate.
 CC !- PATHWAY: Biotin biosynthesis.
 CC !- SUBUNIT: Homodimer.
 CC !- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent aminotransferases.

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OC Vibriaceae; *Vibrio*.
 OC NCBI_TaxID=668;
 RN [1] SEQUENCE FROM N.A.; PubMed=2254256;
 RX MEDLINE=9107226; PubMed=9107226;
 RA Swartzman E., Kapoor S., Graham A.F., Neighen E.A.;
 RT "A new *Vibrio fischeri lux* gene precedes a bidirectional termination
 site for the lux operon.";
 RL J. Bacteriol. 172:6797-6802 (1990).
 -!- FUNCTION: ACYL-PROTEIN SYNTHETASE ACTIVATES TETRADECANOIC ACID.
 CC IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE
 FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS
 SUBSTRATE IN THE LUCIFERASE-CATALYZED REACTION.
 -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 an acyl-protein thioester.
 CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M62812; ; NOT_ANNOTATED_CDS.
 KW Luminescence; Ligase.
 FT NON_TER 1 1
 SQ SEQUENCE 3 AA: 374 MW: 6AA33030000000000 CRC64;
 Query Match Score 6; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 D 4
 Db 3 D 3
 RN [1] RESULT 7
 ACHL_ACHLU ACHLU STANDARD; PRT; 4 AA.
 AC P35904
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DB Achatin-I
 OS Achatina fulica (Giant African snail).
 OC Eukarya; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Siguriatra; Achatinoidae; Achatinidae; Achatina
 NCBI_TaxID=6530;
 RN SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
 RC STRAIN=Perussac; TISSUE=Ganglion;
 RX MEDLINE=9273521; PubMed=2597281;
 RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
 RA Funase K., Sun X.P., Kanapi C.G., Takeuchi H., Nomoto K., Novales-Li P.,
 RA "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
 RT fulica Perussac containing a D-amino acid residue.";
 RT Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
 RN [2] CHARACTERIZATION.
 RP STRAIN=Perussac; TISSUE=Heart atrium;
 RX MEDLINE=91264556; PubMed=1675568;
 RA Fujimoto K., Kubota T., Ynsuda-Kamatani Y., Minakata H., Nomoto K.,
 RA Yoshida M., Harada A., Munehata Y., Kobayashi M.;
 RT "Purification of achatin-I from the atria of the African giant snail,
 RT Achatina fulica, and its possible function";
 RT Biochem. Biophys. Res. Commun. 177:847-853 (1991).
 RN [3] X-RAY CRYSTALLOGRAPHY.
 RP MEDLINE=93014529; PubMed=1399265;

RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
 RA Iwashita T., Nomoto K.;
 RT "Crystal structure and molecular conformation of achatin-I
 RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
 D-amino acid residue.";
 RT Int. J. Pept. Protein Res. 39:258-264 (1992).
 -!- FUNCTION: Neuroexcitatory peptide, increases the impulse frequency
 CC and produces a spike broadening of the identified heart excitatory
 CC neuron (PON); also enhances the amplitude and frequency of the
 CC heart beat. Has also an effect on several other muscles.
 DR PIR; A32480; A32480.
 KW Hormone; D-amino acid.
 FT MOD_RES 2 2
 SQ SEQUENCE 4 AA: 408 MW: 6AADD9C8100000000 CRC64;
 Query Match Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 1 G 1
 RN [1] RESULT 8
 DCML_PSECH DCML_PSECH STANDARD; PRT; 4 AA.
 ID DCML_PSECH
 AC P19916;
 DT 01-FEB-1991 (Rel. 17, Created)
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RT carboxydotrophic bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 CC dioxide.
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -!- COFACTOR: Molybdenum (molybdopterin).
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 RX PIR; PLO140; PL0140.
 KW Oxidoreductase; Molybdenum.
 FT NON_TER 4
 SQ SEQUENCE 4 AA: 7761E876F0000000 CRC64;
 Query Match Score 6; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 G 3
 Db 2 G 2
 RN [1] RESULT 9
 EOST_HUMAN EOST_HUMAN STANDARD; PRT; 4 AA.
 ID EOST_HUMAN
 AC P0731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)

Query Match Score 12; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 3
TRM3_ECOLI TRM3_ECOLI STANDARD PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tram protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID:562;
RN [1]

RP MEDLINE=880227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
and traY genes of plasmid R100";
RL J. Bacteriol. 170:2749-2751(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC -!- PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cyttoplasmic.
CC -!- SIMILARITY: Belongs to the traM family.

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CC DR M20941; -! NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1 1
SEQUENCE 5 AA; 6B1B1AA443500000 CRC64;

Query Match Score 8; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RGD 4
Db 1 KND 3

RESULT 4
TPIS_CANFA TPIS_CANFA STANDARD PRT; 5 AA.
AC P54714;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Fragment).
GN Canis familiaris (Dog).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID:3615;
RN [1]
RP SEQUENCE.

RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J.; Corbett J.M.; Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -!- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
CC Phosphate.
CC -!- PATHWAY: Plays an important role in several metabolic pathways.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the triosephosphate isomerase.
DR HSC-2DPAGE; P54714; DOG.
PROSITE; IPR00652; Triophos_ismre.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_TER 1 1
FT NON_TER 5 5
SQ SEQUENCE 5 AA; 550 MW; 6444862C9A00000 CRC64;

Query Match Score 20.0%; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GN 4

RESULT 5
GRWM_HUMAN GRWM_HUMAN STANDARD PRT; 3 AA.
AC P01157;
ID GRWM_HUMAN
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DB Growth-modulating peptide.
OS Homo sapiens (Human).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID:9606;
RN [1]
RP SEQUENCE.

RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H.; Pickart L.; Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
GO: GO-0001558: P: regulation of cell growth; NAS.
SQ SEQUENCE 3 AA; 340 MW; 6331E8100000000 CRC64;

Query Match Score 6; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 G 3
Db 1 G 1

RESULT 6
LUXE_VIBFI LUXE_VIBFI STANDARD PRT; 3 AA.
ID LUXE_VIBFI
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-Oct-1996 (Rel. 34, Last annotation update)
DE Long-chain fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN LUXE
DB Vibrio fischeri.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibionales;
OC

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:02:23 ; Search time 22 Seconds

(without alignments)
 11.834 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 38

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.4*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	34.3	4	OCP1_OCTMI	P58658 octopus min
2	12	34.3	5	VXA4_CHLTR	P38005 chlamydia t
3	8	22.9	5	TPM3_ECOLI	P13973 escherichia
4	7	20.0	5	TPS2_CANFA	P54714 canis famil
5	6	17.1	3	GRW1_HUMAN	P01157 homo sapien
6	6	17.1	3	GDE2_VIBFU	P24272 vibrio fisc
7	6	17.1	4	ACH1_ACHFEU	P35904 achatin fu
8	6	17.1	4	DQML_PSECH	P19916 pseudomonas
9	6	17.1	4	E0SI_HUMAN	P02731 homo sapien
10	6	17.1	4	OCP3_OCTMI	P58649 octopus min
11	6	17.1	5	AL14_CARM1	P81817 carcinus ma
12	6	17.1	5	B10A_CITTR	P13071 citrobacter
13	6	17.1	5	PAP2_PARMA	P81864 pardachirus
14	6	17.1	5	PEB11_LITRU	P82070 litoria rub
15	6	17.1	5	PEB32_LITRU	P82073 litoria rub
16	6	17.1	5	UF001_MOUSE	P38839 mus musculus
17	5	14.3	4	FAR3_HIRME	P42562 hirudo medi
18	5	14.3	4	FAR4_HIRME	P42561 hirudo medi
19	5	14.3	4	FLRF_HIRME	P58707 anthopleura
20	5	14.3	4	FLRN_ANTEL	P01162 macrocallis
21	5	14.3	4	FMRF_YACNI	P58706 anthopleura
22	5	14.3	4	FYRI_ANTEL	P01858 homo sapien
23	5	14.3	4	FTUF_HUMAN	P41853 artiopoda
24	5	14.3	5	FARP_ARTTR	P01373 periplaneta
25	5	14.3	5	FRCT_PERAM	P19918 pseudomonas
26	2	5.7	4	DCMS_PSECH	P58705 anthopleura
27	2	5.7	4	FEKA_ANTEL	P30425 bothrops in
28	2	5.7	5	BP7_BOTIN	P82071 litoria rub
29	2	5.7	5	FB21_LITRU	P82072 litoria rub
30	2	5.7	5	FE31_LITRU	P80528 zea mays (m
31	2	5.7	5	UC22_MAIZE	P01151 sus scrofa
32	1	2.9	3	THYL_PIG	P58261 daucus caro
33	1	2.9	5	FSK_DAUDA	

ALIGNMENTS

RESULT 1	OCP1_OCTMI	STANDARD;	PRT;	4 AA.
ID	OCP1_OCTMI			
AC	P58658;			
DT	28-PEB-2003 (Rel. 41, Created)			
	28-PEB-2003 (Rel. 41, Last sequence update)			
DB	Cardioactive peptides Ocp-1/Ocp-2.			
OS	Octopus minor (Octopus).			
OC	Bukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoelioidea; Octopodiformes; Octopoda; Incirratata; Octopidae; Octopus.			
NCBI_TaxID	8976;			
OX				
RN	[1]			
SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.				
TISSUE=Brain;				
RX	Iwakoshi E., Hisada M., Minakata H.;			
RT	"Cardioactive peptides isolated from the brain of a Japanese octopus,			
	Octopus minor.";			
RL	Peptides 21:623-630 (2000).			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- PTM: Ocp-2 has L-Phe instead of D-Phe.			
CC	-1- MASS SPECTROMETRY: MW=395.2; METHOD=VALDI.			
KW	Hormone; D-amino acid.			
FT	MOD_RES 2			
SEQUENCE	4 AA; 394 MW; 6AA879C8:1000000 CRC64;			

Query Match	34.3%	Score 12;	DB 1;	Length 4;
Best Local Similarity	100.0%	Pred. No. 1.	1.4e+05	
Matches	2;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	3 GD 4			
Db	3 GD 4			

RESULT 2	UXA4_CHLTR	STANDARD;	PRT;	5 AA.
ID	UXA4_CHLTR			
AC	P38005;			
DT	01-OCT-1994 (Rel. 30, Created)			
	01-OCT-1994 (Rel. 30, Last sequence update)			
DB	Unknown Protein from 2D-page from elementary body (Fragment).			
OS	Chlamydia trachomatis.			
OC	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.			
NCBI_TaxID	813;			
RN	[1]			
SEQUENCE,				
RC	STRAIN=L2/434/Bu;			
RA	Comanducci A., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Christiane G., Birkeland S., Vretclou E., Ratti G., Pallini V.;			
RA	Submitted (SEP-1994) to Swiss-Prot.			
CC	-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 kDa.			
CC	Siena-DRPAGE; P18005; -.			
FT	NON_TER 5			
SEQUENCE	5 AA; 474 MW; 5 75 5			
SQ	75BA865MA800000 CRC64;			

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OM protein - protein search, using sw model

Run on: September 22, 2004, 07:04:09 ; Search time 38 Seconds
 (without alignments)
 12.657 Million cell updates/sec

Title: US-09-912-609-9

Perfect score: 35

Sequence: 1 CRGDC 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing First 45 summaries

Database : PIR_78;*

1: Pir1;*

2: Pir2;*

3: Pir3;*

4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	48.6	5	B45525	actin I - malaria
2	14	40.0	4	S43959	19 mu chain V region
3	14	40.0	5	E22565	R-phyceroerythrin ga
4	12	34.3	4	P07011	T-cell receptor be
5	12	34.3	5	P0689	photosystem I 10.4
6	12	34.3	5	P70513	T-cell receptor be
7	12	34.3	5	P0538	T-cell receptor be
8	12	34.3	5	P0703	T-cell receptor be
9	12	34.3	5	P0690	T-cell receptor be
10	12	34.3	5	P0573	T-cell receptor be
11	12	34.3	5	P0679	T-cell receptor be
12	11	31.4	4	S47552	ubiquitin - rat
13	11	31.4	4	S55238	pallidipin - assas
14	11	31.4	5	A3882	cadmium-binding pe
15	11	31.4	5	P70525	T-cell receptor be
16	11	31.4	5	P70608	T-cell receptor be
17	11	31.4	5	P70695	T-cell receptor be
18	11	31.4	5	P70700	R-phyceroerythrin al
19	9	25.7	3	A22565	metallothionein-A
20	9	25.7	4	I51049	R-phyceroerythrin al
21	9	25.7	5	B22565	hemoglobin, extrac
22	9	25.7	5	S65726	hypothetical prote
23	8	22.9	4	D41654	T-cell receptor be
24	8	22.9	4	P70677	trans-protein - Esc
25	8	22.9	5	A32014	T-cell receptor be
26	8	22.9	5	P70540	spinal cord peptid
27	7	20.0	3	A23751	antho-RFamide neur
28	7	20.0	4	ECXAA	auto-RF amide neu
29	7	20.0	4	A25844	

ALIGNMENTS

RESULT 1

B45525 actin I - malaria parasite (Plasmodium falciparum) (fragments)

C;Species: Plasmodium falciparum

C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000

C;Accession: B45525

R;Wesseling, J.G.; Snijders, P.J.F.; van Soneren, P.; Jansen, J.; Smits, M.A.; Schoenmakers, Mol. Biochem. Parasitol. 35, 167-176, 1989

A;Title: Stage-specific expression and genomic organization of the actin genes of the malarial parasite

A;Reference number: A45525; PMID:89364996; PMID:2671721

A;Accession: B45525

A;Status: Preliminary

A;Molecule type: DNA

A;Residue: 1-5 <WGS>

A;Cross-references: GB:J03988

A;Note: the authors translated the codon GAA for residue 3 as Gly

C;Comment: The actin I gene contains no introns.

Query Match Score 17; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 17; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 17; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

S43959 Ig mu chain V region (clone 13) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C;Accession: S43959

R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajevsky, K.; Nucleic Acids Res. 22, 1389-1393, 1994

A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.

A;Reference number: S43956; PMID:94248036; PMID:8190629

A;Accession: S43959

A;Molecule type: DNA

A;Residue: 1-4 <WAG>

C;Keywords: immunoglobulin

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 14; DB 2; Length 4;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

F22565
 R-phycerythrin gamma-A chain - red alga (*Gastroclonium coulteri*) (Fragment)
 C;Species: *Gastroclonium coulteri*
 C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C;Accession: F22565
 R;Klotz, A.V.; Glazer, A.N.
 J;Biol. Chem. 260, 4856-4863, 1985
 A;Title: Characterization of the bilin attachment sites in R-phycerythrin.
 A;Reference number: A22565; MUID:85182601; PMID:388664
 A;Accession: F22565
 A;Molecule type: protein
 A;Residues: 1-5 <KLO>
 Query Match Score 14; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GDC 5
 Db 1 GTC 3

RESULT 4
 PT0711
 T-cell receptor beta chain V-D-J region (120-2J) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0607; PT0674; PT0678; PT0710; PT0711; PT0710
 R;Feeney, A.J.
 J;Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEF>
 A;Experimental source: adult thymus, strain BALB/c, clone 100-4AL
 A;Accession: PT0606
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE1>
 A;Experimental source: newborn thymus, strain BALB/c, 120-2J
 A;Accession: PT0674
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE2>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 140-1G
 A;Accession: PT0678
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE3>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-1L
 A;Accession: PT0570
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-4 <FE4>
 A;Experimental source: day 19 fetal thymus, strain BALB/c, 141-1I
 A;Accession: PT0711
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4 <FE5>
 A;Experimental source: newborn thymus, strain BALB/c (clones 161-2AE and 161-2AF)
 C;Keywords: T-cell receptor

Query Match Score 12; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 GD 4
 Db 3 GD 4

RESULT 5
 PQ0689
 T-cell receptor beta chain V-D-J region (126-1F) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C;Accession: PT0538; PT0539; PT0603
 R;Feeney, A.J.
 J;Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; MUID:91277601; PMID:1711558
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-5 <FEF>
 A;Experimental source: day 18 fetal thymus, strain BALB/c, clone 126-1F
 A;Accession: PT0539
 A;Status: translation not shown
 A;Molecule type: mRNA

PQ0689
 R-phycerythrin I 10.4K H1 chain - common tobacco (fragment)
 C;Species: *Nicotiana tabacum* (common tobacco)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999

A;Residues: 1-5 <FB2>
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AC
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 8
PT003
T-cell receptor beta chain V-D-J region (135-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
A;Accession: PT0703
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0309; PMID:91277601; PMID:1711558
A;Accession: PT0703
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FB2>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 9
PT090
T-cell receptor beta chain V-D-J region (140-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
A;Accession: PT0690
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0309; PMID:91277601; PMID:1711558
A;Accession: PT0690
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FB2>
A;Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 10
PT0573
T-cell receptor beta chain V-D-J region (141-1CC) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PT0573
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0573
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <FB2>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 11
PT0579
T-cell receptor beta chain V-D-J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
A;Accession: PT0679; PT0708
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; PMID:91277601; PMID:1711558
A;Accession: PT0679
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FB2>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Accession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FB2>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor

Query Match 34.3%; Score 12; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GD 4
Db 3 GD 4

RESULT 12
S47552
ubiquitin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 17-Mar-1999
C;Accession: S47552
R;Hubbard, M.J.; Carne, A.
Biochim. Biophys. Acta 1200, 191-196, 1994
A;Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in rat
A;Reference number: S47552; PMID:94304928; PMID:8031840
A;Accession: S47552
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <HQB2>

Query Match 31.4%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RG 3
Db 2 RG 3

RESULT 13

S55238 pallidipin - assassin bug (fragment)

C;Species: Triatoma pallidipennis (assassin bug)

C;Date: 19-Mar-1997 #sequence_revision 11-Jul-1997 #text_change 19-May-2000

C;Accession: S55238

R;Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleuniger, J.

Biochem. J. 265:470, 1995

A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhibitor

A;Reference number: S55238; PMID:773384

A;Accession: S55238

A;Molecule type: protein

A;Residues: 1-4 <HAE>

Query Match Score 11; DB 2; Length 4;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DC 5

Db 2 EC 3

RESULT 14

A33882 cadmium-binding pentapeptide - downy thornapple

C;Species: Datura innoxia (downy thornapple)

C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993

C;Accession: A33882

R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.

Proc. Natl. Acad. Sci. U.S.A. 84: 6619-6623, 1987

A;Title: Poly(Gamma-glutamylcysteinyl)Glycine: its role in cadmium resistance in plant c

A;Reference number: A94182; PMID:347793

A;Accession: A33882

A;Molecule type: protein

A;Residues: 1-5 <JAC>

Query Match Score 11; DB 2; Length 5;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DC 5

Db 1 EC 2

RESULT 15

PT0525 T-cell receptor beta chain V-D-J region (100-4J) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PT0525

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; PMID:91277601; PMID:1711558

A;Accession: PT0525

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <PEE>

A;Experimental source: adult thymus, strain BALB/C

C;Keywords: T-cell receptor

Query Match Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RG 3

Db 3 RG 4